

[illegible][illegible]



[illegible][illegible]

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 Db 479 gccaa 482
 RESULT 9
 AA33777
 ID AA233777 standard; cDNA; 605 BP.
 AC AA233777;
 XX 09-DRC-1999 (first entry)
 DT
 XX Tobacco plant resistance-associated cDNA fragment 102.
 DE
 XX Tobacco; plant; resistance; tobacco mosaic virus; TMV; infection;
 KW protection; plant protection agent; phytopathogenic fungi; nematode;
 KM insect pest; pathogen resistance; transgenic plant; diagnosis; ss.
 XX Nicotiana tabacum.
 OS
 XX DE19813048-A1.
 PN 30-SEP-1999.
 XX
 PD 25-MAR-1998; 98DE-1013048.
 XX
 PF 25-MAR-1998; 98DE-1013048.
 XX
 PR 25-MAR-1998; 98DE-1013048.
 XX
 PA (FARB) HAYER AG.
 XX
 PI Schreier P, Garbers C, Langen G, Kiedrowski S;
 XX
 DR WPI; 1999-552163/47
 XX
 P1 Nucleic acids useful for identifying compounds capable of inducing
 P1 pathogen resistance in plants
 P1
 P5 Claim 1a: 66; 130pp; German.
 XX
 CC This invention describes novel cDNA molecules corresponding to tobacco
 CC (Nicotiana tabacum) genes that are expressed in response to tobacco
 CC mosaic virus (TMV) infection. Regulatory regions that provide specific
 CC expression of the nucleic acids in connection with induced resistance
 CC can be used to identify compounds useful for plant protection by
 CC transforming a cell with a recombinant DNA molecule containing a
 CC selectable and/or detectable marker linked to the regulatory region,
 CC culturing the cell in the presence of a test compound or sample, and
 CC identifying a compound or sample that suppresses or activates and/or
 CC enhances expression of the marker. Host cells containing the nucleic
 CC acid, or polypeptides encoded by the nucleic acids, can be used to
 CC identify compounds that inhibit or activate a polypeptide involved in
 CC induced resistance, by contacting the cell or polypeptide with one or
 CC more test compounds and identifying compound(s) that specifically
 CC modulate the activity of the polypeptide. Plant protection agents can be
 CC prepared by formulating the identified compounds in a form suitable for
 CC their uptake and optionally metabolism in organisms, especially
 CC plants, phytopathogenic fungi, nematodes or insect pests. The nucleic
 CC acids or regulatory regions, or corresponding vectors, or the
 CC polypeptides encoded by the nucleic acids, or compounds identified as
 CC above, can be used to improve the pathogen resistance of plants or to
 CC produce transgenic plants. The nucleic acids or regulatory regions, or
 CC vectors, cells, plants or plant tissues containing them, or the

CC polypeptides and antibodies to the polypeptides, can be used to screen
 CC for new plant protection agents or genes involved in induction of
 CC resistance in plants. Vectors containing the nucleic acids, or the
 CC regulatory regions or recombinant DNA molecule or vectors containing
 CC them, or the compounds identified as above, or the polypeptides or
 CC antibodies, can be used in diagnostic compositions. AA234676-23888
 CC represent fragments of tobacco cDNA which are associated with plant
 CC resistance.
 XX
 SO Sequence 605 BP; 169 A; 105 C; 137 G; 194 T; 0 other.
 Query Match 10.6%; Score 142.8; DB 20; Length 605;
 Best Local Similarity 71.1%; Pred. No. 3.2e-19;
 Matches 189; Conservative 0; Mismatches 77; Indels 0; Gaps 0;
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 AAA96460
 ID AAA96460 standard; DNA; 207 BP.
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 AC AAA96460;
 XX
 CT 08-FEB-2001 (first entry)
 XX
 DE Nucleotide sequence of the promoter Mpi1098.
 XX
 KM petE promoter; chimeric promoter; transgenic plant; Mpi1097;
 KM plastocyanin gene promoter; ss.
 XX
 OS Synthetic.
 OS Pisum sativum.
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 PN W020056906-A1.
 XX
 PP 28-SEP-2000.
 XX
 PF 20-MAR-2000; 2000W0-1800317.
 XX
 PP 22-MAR-1999; 98FP-0003635.
 XX
 FA (MERT-) MERISTEM THERAPEUTICS.
 XX
 PI Rance I, Gruter V, Theissen M;
 PI
 DR WPI; 2000-587067/55.
 XX
 PT Chimeric expression promoter for producing divyaledonous and
 PT monocultedonous transgenic plants comprises a nucleic acid sequence
 PT derived from a promoter of the pea plastocyanin gene
 XX
 P5 Claim 2; Page 67; 83pp; English.



ACCESSION	HCA57563
VERSION	HCA57563.1
KEYWORDS	GI:1380804
SOURCE	EST
ORGANISM	Bareil medic.
JOURNAL COMMENT	Medicago truncatula Eudayotia, Viridiplantae; Streptophyta, Embryophyta; Tracheophyta; Spermatophyta, Magnoliophyta; eudicotyledons, core eudicots; Rosidae; eurosoids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago. 1 (bases 1 to 637) Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,J.J., Flores, H.R., Imman,J.T., Weller,J.W., May,G.D., and Harrison,M.J. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula phosphate-starved leaf library Unpublished (2006) Contact: Harrison MJ Plant Biology Division The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7325 Fax: 580 221 7380 Email: mharrison@noble.org Insert length: 637 std error: 0.00 Plate: 105 row: G column: 07 Seq primer: TCACACAGCAACACTATGAC. location/Qualifiers 1..637 /organism="Medicago truncatula" /db_xref="taxon:3880" /clone="Np105C07P1" /clone_lib="phosphate starved leaf" /tissue_type="leaf" /dev_stage="trifoliolate" /note="Vector: Lambda Zap; At the trifoliolate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 hoaglands solution containing only 20uM potassium phosphate. RNA was prepared from above ground tissues." BASE COUNT 178 a 148 c 128 g 182 t 1 others ORIGIN
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Best Local Similarity	95.4%; Pred.No. 1.2e-61;
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Db 360 ATGGGGCTTTGGCTTTTGGTCCAAACAAATTGATGCTGCAACCGCTGACACAGCAATACAT 419
Cy 1266 :CAAGACAAATAGCGATGCTTCTTCTAGATGTTACTCTTATGAGAGAGAGAGATCTGAG 1425
nb 420 TCAAAATCAATATGTTGATTTCTCTCAAAATGTAATCTTGATGTAAGAAAGCAATTCGAAAG 479
Cy 1326 GAGTTGATGCTGCAAA 1340
Db 480 GGGTGATGACAGCA 494

RESULT 4
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LOCUS BE249400
DEFINITION NP014406EF1058, developing leaf Medicago truncatula cDNA clone
ACCESSION NP014406EF1058, mRNA sequence.
VERSION BE249400
KEYWORDS BE249400.2 GI:11959244
SOURCE EST.
ORGANISM Medicago truncatula
barrel medic.
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales;
Medicago.
1 (bases 1 to 483)
Torres-Jerez, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula leaf library
Unpublished (2000)
On Jul 13, 2000 this sequence version replaced gi:119461.
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Medicago Genome Initiative accession: MGIS14974
Insert Length: 671 Std Error: 0.00
Plate: 014 ROW: F column: 06
Seq primer: TCAACAGCAAGCAACGTAATAC.
location/Qualifiers
1..483
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NP014406EF"
/contig="lib2developing leaf"
/tissue_type="leaf"
/rev_stage="Pooled developmental"
/notes="Vector: Lambda ZAP, Contains a mixture of very
young, developing, mature and senescing leaves."
FASL COUNT 131 a 112 c 95 g 141 t
ORIGIN

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Country Match	27.00%	Score: 3.75, 4.13, 10.2	Length: 5, 10, 2
Host Local Similarity	97.20%	Prod. No.: 4, 50, 6, 2	
Matches: 422	Consistent: 112	Invalid: 02	GPS: 02

Neofutism	"Model of a futuristic city"	1.64	0	1.22	0	1.22	0	1.55
Abstrct	"Abstract drawing"							
Octonoe	"Neofut of a P"							
Octonoe	"The 'developing' level"							
Tissue type	"Leaf"							
Adv. stage	"Isolated development"							
Proto vector	"lambda ZAP contains a mixture of very young, developing, mature and senescent viruses"							

[illegible]

NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Policy & Parliamt
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM ps/compatile
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,464
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/87/945,414
FILING DATE:
APPLICATION NUMBER: EP 91 114 400,6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BERT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/CITATIONS: 2042,114 1MM0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)846 9400
TELEFAX: (703)684 4109
TELEX: 869149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 72th base pairs
TYPE: nucleic acid
STRAND/INESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ19+FLS
US-08-232,464-FLS

[illegible]


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DB 78 TAATAATTAACTAAATAATTAATAAATAAAGTTATATTAATGCTTTAATAATTA
RBSJLT 6
US-J8-998-416-1137
: Sequence 1137, Application US/08998416
: Patent No. 6239264
GENERAL INFORMATION:
: APPLICANT: Pihlpsen, Peter
: APPLICANT: Pohlmann, Rainer
: APPLICANT: Steiner, Sabine
: APPLICANT: Mohr, Christine
: APPLICANT: Wendland, Jurgen
: APPLICANT: Knechtle, Philipp
: APPLICANT: Redischung, Corinne
: TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHVA GOSYPII
: TITLE OF INVENTION: AND USHS THEREOF
: NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESSES:
: ADDRESSEE: No. 6239264ar1s Corporation
: STREET: 3054 Cornwallis Road
: CITY: Research Triangle Park
: STATE: No. 6239264Ar1 Carolina
: COUNTRY: USA
: ZIP: 27709
COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent release #1.0, Version #1.30
CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/998,416
: FILING DATE: 24-DEC-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION NUMBER:
: APPLICATION NUMBER: CH 00016/97
: FILING DATE: 31-DEC-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Meigs, J. Timothy
: REGISTRATION NUMBER: 38, 241
: REFERENCE/DOCKET NUMBER: P/75-30306/A/CCT1976
TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-541-8587
: TELEFAX: 919-541-8689
: INFORMATION FOR SEQ ID NO: 1137:
SEQUENCE CHARACTERISTICS:
: LENGTH: 636 base pairs
: TYPE: nucleic acid
STRANDEDNESS: single
: TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
: ORGANISM: PAG1692RF
US-08-998-416-1137
Query Match 4.4%; Score 58.8; DH 4; Length 636;
Best Local Similarity 45.5%; Pred. No. 2.4e-05;
Matches 245; Conservative 0; Mismatches 292; Indels 1; Gaps 1
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Q7 248 gaggagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaag 307
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RESULT 7
US-08-446-855A-1
Sequence 1, Application US/08446855A
Patent No. 5849573
GENERAL INFORMATION:
APPLICANT: Stewart, Thomas S
APPLICANT: Flores, Maria V
APPLICANT: O'Sullivan, William J
TITLE OF INVENTION: Nucleotide sequence encoding carboxyl
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: Nixon & Vanderye PC
STREET: 1100 No. 5849573th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patchin Release #1.24
CURRENT APPLICATION DATA:
APPL-ALL-N NUMBER: US 58-446-855A
FILING DATE: 06-30-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard G
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 47-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
FAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8920 base pairs
TYPE: nucleic acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic
US-08-446-855A-1
Query Match 1.2% Score 57.2; Dh 2; Length 8920;
Best local Similarity 46.1%; Prod No 0.00015;
Matches 226; Conservative 0; Mismatches 269; Indels 1; Gaps 1;
52 aaagatllaaagtlaaagaaagatgtaacatttattttaaataaataatattaaactaaact 111

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GenCorp version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 1, 2002 00:54:34 : Search time 413.71 seconds
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4941301 Million cell updates/sec

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Scoring table:
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Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
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Post-processing: Minimum Match 98
Maximum Match 100%
Listing first 45 summaries

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16: em_fun:*
17: em_hum:*
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pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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No. Score Match Length DB ID Descr: plon

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15	89	9.2	296	6	AX036603	AX036603 Sequence
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25	79.6	8.2	1987	3	EDIRAP1A	EDIRAP1A
26	79.2	8.2	496	6	AL52982	AL52982
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ALIGNMENTS

RESULT 1	AX105268	971 bp	UNA	100%	100%	100%
DEFINITION	Sequence 2 from Patent WO0125455					
ACCESSION	AX105268					
VERSION	AX105268.1	51:13921418				
KEYWORDS						
ORGANISM	synthetic construct.					
SOURCE	synthetic construct.					
REFERENCE	1 (bases 1 to 971)					
AUTHORS	Veizina, L.P. and D'Aoust, M.A.					
TITLE	Promoter for regulating expression of foreign genes					
JOURNAL	Patent: WO 0125455 A 2 12-Apr-2001;					
Medicago Inc. (CA)						
FEATURES	Location/Qualifiers					
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BASE COUNT 390 a 141 c 145 g 275 t
ORGANISM "synthetic construct"
/dd_xref="taxon:32630"
/note="Sequence to be used as a promoter for regulating expression"

Db	609	CGATGAGTTCAGTAACTATTATTATATTTCATGATTAATTAAGATCAAAATACGATAT	668
Qy	661	attaatccctcccaaaaaaaacggtatataattcctaaaaaatctaugccagctagag	720
Nb	669	ATTATCCCTCCCAAAAAAAMAAACGGATATATTACIAAAAAAATCAACCCACGGTAGCG	728
Qy	721	gataacatccatcccaacccaacacacacccctgataagataaccacgttaaacccac	780
Db	729	GATACATACCAATCCAACTAATCCAAACCAATCCCTCATAGATTAACCCATTTAAACCCAC	788
Qy	781	gcactctgtgcacatctcatatctaatctaacatctcttcacacatctctgacaca	840
Nb	789	GACCTCTGTGGACATCTCAATATATCTAAATCAACACATCTCTCCACAACTCTGAGCGACA	848
Qy	841	caaaaaaccaatccacatctttatcccatctataaaaaatccacacttctgtgactac	900
Nb	849	CAAAAACCAATCCACATCTTTATTCACCAATCTATAAAAAATCCACACCTTTCGACCTCAC	908
Qy	901	acttltgattcccttcaaacacatcaaaagagagagatctaatlaattaatcatctt	960
Nb	909	ACTTTGATTCCCTTCAAAACACATACCAAGAGACAGACIAATTAATTAATTAATCACTCT	968
Qy	961	gagagaaaaatg 971	
Db	969	GAGAGAAAATG 979	

[illegible]

	Query Match	75.3%	Score 731	DB 6	Length 731	
	Best Local Similarity	100.0%	Prod No. 4	6e-107		
	Matches 731	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
QY	241	agagagaaaaggaagaagagataaaacataatgttgatgatagagaaagtgtga	300			
Db	1	ACAGCGAAAAAGCAGACACCGACAGATAAAAACATAATGTCGATGACACAGCAAAAGTGTGA	60			
OY	301	caaaaggttaccacaatatglttacaatatcatlgaagatlttgcaaaagctacaa	360			
DE	61	CAAAAGTTCTACCAAAATAGTTGTACAAATATCATTTACGAATTTTGACAAAAGCTACACA	120			
OY	361	aataagggtaatgctgttaataataagaatgacatagagafatgaaccattaga	420			
DE	121	AATAAGGGTAAATTCCTGTAAATAAATAAGGATATATATTCATGATGATGTTCATTAGA	180			
OY	421	gaatttttggcaagtcattaaaagagaaagataaattatctttaaataaaagttgatt	480			
DE	181	GAAATTTTGGCAAGTCATATAAAAACAAGAAATAAATATTTTAAAAATTTAAAGCTTGACT	240			
OY	481	catttgattaaacatgattattcaatgaattgataaaagtttgaattaaagtgtat	540			

Dh	241	CATTGATTAACAGTGTATTATTATTTAAATGATSTATGAAGAAGTGATTAAGTTGAT	800
OY	541	TatTaattagaatttgggtgccaatttaattgaacatttgatctttcctaataatagcc	609
Dh	301	TATGATTTGAAATTTGGTGTCTCAATTTAATTGNAATTTTCATTTTTCATAATATCCG	360
OY	601	cCaagaactgcgaacaactcttttatatttcacagatcaaaagaagaadaaaggat	460
Dh	361	CCATTAGAGCAGCTTAACGCATTTTTATATTTTCATACATCGAAATACACAATAAACGGAT	420
OY	661	attaaccctccaaaaaaaaacccgatatttaactaaaatctaagcccgtagag	720
Dh	421	ATTATTCCTCTGAAAAAAAACAGGATATATTTACTAAAAATCTAAAGTACGGTAAGS	480
OY	721	tataaaccttcgaatcccacacgaatcacacgaatgcgaatatgaatgaaggaattgaag	780
Dh	481	GATTAACATGCCAAATCCAAACAAACAAACAAACAAACAAATGCTATGATAGACCTTAACGCGAC	540
OY	781	gaacctctgagagacatacatcatatctdaadtaacacattctccagatctgaagtga	840
Dh	541	GCACCTGTGGCACATCTACATTAATCAAAATCACACATCTCTCCACACATCTGACGCCACA	600
OY	841	caaaaaccaalccacatctttaaccacactctataaagaacacacatttgaaatcac	900
Dh	601	CAAAAAACATATACATCTTTTATCAACCAATCTATATAAAAAATCAACACCTTGGAGCTAC	660
OY	901	aatttgattccctcaaacacatacaagagagagagataattaatattaatatcctt	960
Fd	661	AATTGATTTCTTTTAAAT	720
OY	961	gagagaanaal 971	
Dh	721	SACACAAAATC 731	

LOCUS	AX036596	623 bp	DNA	Insert	PAI 16 NOV-2000
DEFINITION	Sequence 2 from patient H279138				
ACCESSION	AX036596				
VERSION	AX036596.1	GI:11226191			
KEYWORDS					
SOURCE					
ORGANISM	Synthetic construct; synthetic construct; artificial sequence.				
REFERENCE	1 (bases 1 to 623)				
AUTHORS	Rance, I., Theisen, M. and Guber, V.				
TITLE	Patient: FR 279138-A 26-SEP-2000;				
FEATURES	MERISTEM THERAPEUTICS (FR)				
SOURCE	Location/Qualifiers				
	1..623				
	/organism="synthetic construct"				
	/db-arch="taxon:5630"				
	1..623				
Promoter	/note="Promoter MPr1097 derived from the promoter pMPr1097 a deletion in 5' of the repeated invert sequences as well as the as-1 like box borne on fragment SpH1 of 212 bp promoter MPr1097"				
BASE COUNT	230 a 128 c 82 g 183 t				
ORIGIN					
Query Match	19.8%	Score 191.8;	DB c	Length 623;	
Best Local Similarity	82.8%	Prod. No. 1190-21;			
Matches 231; Conservative	0; Mismatches 477	Indels 1;	Gaps 1;		
DB	321 AAAATATACACTACTATTATTACTAAAAAAATCTAAGCCACGTCGACGATACACATCA 380				
QY	733 TCGAACCAATACGAAGATCTGATGAGTAACTGATTAAGTTCGAGGACTGTGAT 732				

certain photoregulated genes is modulated by phosphorylation. The
Plant Cell 1, 1069-1077, 1989).

FEATURES

source

Location/Qualifiers
1..998
/organism="Pisum sativum"
/cultivar="Peltam First"
/db_xref="taxon:3888"
/clone="pPCPC1"

repeat_region 174..236
repeat_region 208..232
repeat_region 224..242
repeat_region 246..251
repeat_region 267..299
repeat_region 301..316
repeat_region 317..332
repeat_region 333..351
misc_feature 353..360
misc_feature 363..360
misc_feature 401..417
misc_feature 698..709
misc_feature 739..746
misc_feature 857..870
misc_feature 903..910
TATA_signal 940..958
mRNA
gene 940..998
CDS 993..998
/gene="pele"
/codon_start=1
/product="plastocyanin"
/protein_id="CAA48393.1"
/db_xref="GI:4379383"
/translation="MA"
BASE COUNT 339 a 201 c 154 g 304
ORIGIN

Query Match 18 58; Score 179.4; DH 8; Length 998;
Best Local Similarity 60.98; Pred. No. 1.6e-19;
Matches 326; Conservative 0; Mismatches 206; Gaps 3; Gaps 2.

417 tagagaatttggcaagcattataaagaagaataattatcttaataataagct 476
446 TAAGAGACCTCTTAAACATACCACTTTCAGTCTTGAATATAGCTAATAAGATG 505
477 gaacattgataaacaagatgattatgaatgaatgaagaagatgattaaagt 536
506 AACTCATATATATATGAAAGCAATATGCAACCAACCAACCAACCAACCAACCA 565
537 gatttgtaataagatttggatgataatgaatgaatgaatgaatgaatgaatga 596
566 TAAACACCAATCTTGTATATATATATATATATATATATATATATATATATAT 625
597 tggccatagatgattgaatgaatgaatgaatgaatgaatgaatgaatgaatga 656
626 ATTCTCCGAT 685
657 gataatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 716
686 GCAAGTACGAGAAAT 745
717 gggagataaataatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 776
746 GGAAGAT 805
777 caagcactctggtgacatctacattatataatgaatgaatgaatgaatgaatga 836
|||||

DB 806 CCACGACATCTGCGACATATATATATATATATATATATATATATATATATAT 865
QY 837 caacaaaaa-ccatccatcttatacccatctataaaaaa-ccatcttgaag 895
DB 856 CANN-MAAA-CAATCTTGAATATATATATATATATATATATATATATATATAT 924
QY 895 tctaacatttgcctccatcaacacacacacacacacacacacacacacacacac 950
EB 924 TCTCTTTCAT 978

RESULT 8
PSPIAS
LOCUS PSPIAS 1505 bp DNA linear JUN 27 MAR 1995
DEFINITION pea gene for plastocyanin.
ACCESSION X16082
VERSION X16082.1 GI:20845
KEYWORDS electron carrier; photosynthesis; plastocyanin.
SOURCE pea.
ORGANISM Pisum sativum
Eukaryota; Viridiplantae; Streptophyta; Etrichophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;
Pisum.
REFERENCE 1 (bases 1 to 1505)
Last, D.L. and Gray, J.C.
Plastocyanin is encoded by a single copy gene in the pea haploid
genome.
JOURNAL Plant Mol. Biol. 12, 655-666 (1989)
FEATURES
source location/Qualifiers
1..1505
/organism="Pisum sativum"
/strain="Peltam First"
/db_xref="taxon:3888"
/clone="lambda gpc3"
/tissue_type="shoots"
/clone_id="lambda EMU13"
1..46
/note="imperfect direct repeat 1"
21..50
/note="imperfect direct repeat 2"
25..62
/note="imperfect direct repeat 3"
39..41
/note="aca was aga in [1]"
/citation=[1]
59..88
/note="imperfect direct repeat 2"
94..119
/note="imperfect direct repeat 1"
114..142
/note="imperfect direct repeat 2"
130..159
/note="imperfect direct repeat 2"
134..171
/note="imperfect direct repeat 3"
723..730
/note="TATA box"
758..761
/note="put. transcriptional start site"
813..1319
/note="precursor peptide (AA -69 to 99)"
/codon_start=1
/protein_id="CAA48393.1"
/db_xref="GI:20846"
/db_xref="SWISS-PROT:P16002"
/translation="MALVISIYVAIPSTSLKMAATKASAMAKIETLSISQRIQV
ASLKPDAVAIAASAVASNAIAAVVILGASIGASVPSLSASQRIYFQANA
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MVGQVTN"
813..1019
transit_peptide
1020..1316
misc_feature
/product="mature plastocyanin (AA 1-99)"




```

OY 181 ttgttgcacatttgagaaatttgtgtctctcttcatttgatgacaaagaaatag 240
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Db 189 ttgttgcacatttgagaaatttgtgtctctcttcatttgatgacaaagaaatag 248
OY 241 agagagaaagagagagagagagagagagagagagagagagagagagagagag 300
    |||
Db 249 agagagaaagagagagagagagagagagagagagagagagagagagagagag 308
OY 301 caaaatttgacaaatattgttgcacatttgagagagagagagagagagagag 360
    |||
Db 309 caaaatttgacaaatattgttgcacatttgagagagagagagagagagagag 368
OY 361 aataagagagagagagagagagagagagagagagagagagagagagagagag 420
    |||
Db 369 aataagagagagagagagagagagagagagagagagagagagagagagagag 428
OY 421 gaattttggcagatcatttaaaagagagagagagagagagagagagagag 480
    |||
Db 429 gaattttggcagatcatttaaaagagagagagagagagagagagagagag 488
OY 481 cattgattaaacatgagatatttaagagagagagagagagagagagagagag 540
    |||
Db 489 cattgattaaacatgagatatttaagagagagagagagagagagagagagag 548
OY 541 tagtaattagaatttggatgacaaatttaattgacatttgatcttctatattgc 600
    |||
Db 549 tagtaattagaatttggatgacaaatttaattgacatttgatcttctatattgc 608
OY 601 cctagagtcagatcattcattttatatttcataagacaaatagagaaatagag 660
    |||
Db 609 cctagagtcagatcattcattttatatttcataagacaaatagagaaatagag 668
OY 661 attaaacccccaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaa 720
    |||
Db 669 attaaacccccaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaa 728
OY 721 gataacatccaatccaacatccaacatcccgatgagagagagagagagagagag 780
    |||
Db 729 gataacatccaatccaacatccaacatcccgatgagagagagagagagagagag 788
OY 781 gcaatctggcagatcattcattatcattatcattatcattatcattatcatt 840
    |||
Db 789 gcaatctggcagatcattcattatcattatcattatcattatcattatcatt 848
OY 841 caaaacccaatccaatccaatccaatccaatccaatccaatccaatccaatcca 900
    |||
Db 849 caaaacccaatccaatccaatccaatccaatccaatccaatccaatccaatcca 908
OY 901 acttgatcccttcaacatcacaagagagagagagagagagagagagagagag 960
    |||
Db 909 acttgatcccttcaacatcacaagagagagagagagagagagagagagagag 968
OY 961 gagagaaatg 971
    |||
Db 969 gagagaaatg 979

```

```

RESULT 3
AAS02128
ID AAS02128 standard, DNA, 731 bp.
XX:
AC AAS02128:
XX:
D7 18-JUL-2001 (first entry)
XX:
D3 Promoter #3 for regulating expression of foreign genes.
XX:
KY Promoter, transgenic plant, monocotyledon; dicotyledon; gymno-perm; ds
XX:
O3 Synthetic.
XX:
PN WO200125455-A2.

```

```

XX 12-APR-2001.
XX
XX C2-OCT-2000; 2000W CA01144.
XX
XX 04-OCT-1999; 99US-0157129.
XX
XX (MEDT-) MEDICAGO INC.
XX
XX Vezina L, F'roust M.
XX
XX WP1: 2001-266315/27.
XX
XX Novel promoter for regulating expression of foreign genes in transgenic
XX plants, more specifically in a leaf-specific manner in transgenic
XX plants.
XX
XX Claim 1: Page 9; 9pp; English.
XX
XX The sequence represents the coding sequence of promoter #3 for regulating
XX expression of foreign genes in transgenic organisms. The promoter is
XX useful for regulating the expression of foreign genes in transgenic
XX organisms, particularly plants, e.g. monocotyledons, dicotyledons or
XX gymnosperms, by preparing a transgenic organism using an expression
XX construct comprising the promoter and an open reading frame (ORF) of a
XX gene.
XX
XX Sequence 731 BP; 299 A; 115 C; 109 G; 210 T; 6 other.
XX
Query Match 75.3%; Score 731; DH 22; Length 731;
Host Local Similarity 100.0%; Pctd. No. 3, 5c-121;
Matches 731; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 241 agagagaaagagagagagagagagagagagagagagagagagagagagagag 300
    |||
Db 1 agagagaaagagagagagagagagagagagagagagagagagagagagagag 60
OY 301 caaaatttgacaaatattgttgcacatttgagagagagagagagagagagagag 360
    |||
Db 61 caaaatttgacaaatattgttgcacatttgagagagagagagagagagagagag 120
OY 361 aatagaggttaattgtgtgaatgaatgaatgaatgaatgaatgaatgaatgaat 420
    |||
Db 121 aatagaggttaattgtgtgaatgaatgaatgaatgaatgaatgaatgaatgaat 180
OY 421 gaattttggcagatcatttaaaagagagagagagagagagagagagagagag 480
    |||
Db 181 gaattttggcagatcatttaaaagagagagagagagagagagagagagagag 240
OY 481 cattgattaaacatgagatatttaagagagagagagagagagagagagagagag 540
    |||
Db 241 cattgattaaacatgagatatttaagagagagagagagagagagagagagagag 300
OY 541 tagtaattagaatttggatgacaaatttaattgacatttgatcttctatattgc 600
    |||
Db 301 tagtaattagaatttggatgacaaatttaattgacatttgatcttctatattgc 360
OY 601 ccaatagagtcagatcattcattttatatttcataagacaaatagagaaatagag 660
    |||
Db 361 ccaatagagtcagatcattcattttatatttcataagacaaatagagaaatagag 420
OY 661 attaaacccccaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaa 720
    |||
Db 421 attaaacccccaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaa 480
OY 721 gataacatccaatccaacatccaacatcccgatgagagagagagagagagagag 780
    |||
Db 481 gataacatccaatccaacatccaacatcccgatgagagagagagagagagagag 540
OY 781 gcaatctggcagatcattcattatcattatcattatcattatcattatcatt 840
    |||
Db 541 gcaatctggcagatcattcattatcattatcattatcattatcattatcatt 600

```

[illegible]

RESULTS

(1)	AAA96d ^a ,B standard; INA, O.A.B.
XX	
A'	AAA96d ^a ,B;
XX	
OI	OM FEB 2001 (first entry)
XX	
DCE	Nucleotide sequence of the promoter M7-109?

FW	pot E promoter, plasmid for E. coli	2	transgenic plant: MP1109/2
KW	plastic cyanide gene promoter	38	
XX	SyrB promoter	35	
XX	Plum salt toxin	38	
XX	Wt2000-6-906 A1	38	
XX	28 SEP 2000	38	
XX	20 MAR 2000: 2000W-1800-1	38	
XX	22 MAR 1999: 04PK 0006-3	38	
XX	(MORI) MEKISTEY THEKAROT 35	38	
XX	Kanoe 1, 1700g V, 110-150 M	38	
XX	WPI: 2000 587667/55	38	
XX	chromosome expression promoter for producing direct cytosolic and	38	
XX	transmembrane proteins. Transgenic plants comprises a nucleotide acid sequence	38	
XX	derived from a promoter of the pea plastocyanin gene	38	
XX	claim 2: page 66: 84pg finalish	38	

The present sequence represents the chimeric promoter *Ma1009*. The promoter is derived from the *psfE* promoter from *psa* plastocyanin gene, by a deletion in 5' of the repeated invert sequences as well as the *psfE* as 1 like box located on a 5' to 3' fragment of 212 bp. The *psfE* promoter directs cell specific but not full light-regulated expression in *transgenic tobacco plants*. The promoter is used to construct chimeric promoters of the invention. The specification describes a chimeric expression promoter comprising a promoter of the *psa* plastocyanin gene, or comprising a *box* operably or functionally linked upstream of a CAAT *box*, TATA *box* and transcription initiation site. The chimeric promoters are used in expression vectors for producing *transgenic plants*, such as dicotyledonous species, and *prokaryotic*, *eubacterial*, *actinobacteria*, *fungi*, *metallophytes*, *yeast*, *algae*, *protozoa*, or *nonflowering* and *monocotyledonous* species, *of a whole*, *cell*, *tissue*, or *organ*.

Query Match	Score	Length					
Most Local Similarity	82.8%	Protd. No. 1, 56, 2%					
Matches	241	Mismatches	47	Indels	1	Gaps	1

[illegible]

RESUME

III	AAA96457	Standard; DNA; 864 bp.
XX		
XX	AA96457;	
XX		
XX		
XX	08-FEB-2001	(TTTSTCTT7)
XX		
XX		

XX Nucleotide sequence of the petE promoter from plastocyanin gene.
XX
KM petE promoter; chloroLc promoter; Transposon Frame;
KM plastocyanin gene promoter; ssr.
XX
XX
08 pIsun sat frame.
XX
FN W020056906 A1.
XX
PD 28 SEP 2000.
XX
XX
XX 20 MAR 2000; 2000W0-1B00417
XX
XX 22 MAR 1999; 99FR 0005635.
XX
XX (MERIT-) MERISTEM THERAPEUTICS
XX
P1 Katoch I., Grotzer V., Lichten M.
XX
XX Wf1; 2000-087667/55.
XX
XX
XX Chlorite expression promoter for producing diacylglycerols and
PT monoterpenoids. Transgenic plants comprising a complete seed sequence
P1 derived from a promoter of the psn plastocyanin gene
XX
XX Claim 1; Page 65; B type; English

cc The present database represents the pool of promoters from the *pot* plastogenin gene, the promoter directs cell-specific but not full cell light-regulated expression in transgenic tobacco plants. The promoter is used to construct chimeric promoters of the present work. The specification describes a chimera expression promoter comprising a promoter of the *pot* plastogenin gene, an enhancer, a 5' box operably or functionally linked upstream of a *GAL4* box and a transcription initiation site. The chimera promoters are used in expression vectors for producing transgenic plants, such as directly endogenous species, e.g., potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea, rape, beetroot, or sunflower, and nontransgenic species, e.g., wheat, barley, oat, rice, or corn.

Query Match	19.08	Score [0.38	18.21	Count	0.04
Host Local Similarity	02.00%	Prod. Mo.	1.50	27	

Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicotyledons: Rosales: euforbiids: Fabales: Fabaceae: Papilionoideae: Luteolaceae

THESE

Authors
 Bourne, E. P., Tresselt, R., van Tuinen, D., Gonyea, J., Jallion, C.,
 Nichol, A., Carreau, V., Chaliquier, A., Kahn, D., Gianninazzi, P., and
 Peatston

Medicine University of Tokyo, Tokyo, Japan

Journal of Applied Linguistics 41 (2000)

Microscopio - Centro Nacional de Sequenciadores

Find it: Seeq and iQueued

$$COT(\mathcal{A}) = \{A_1, \dots, A_n\} \text{ and } H(\mathcal{A}) = \{M_1, \dots, M_n\} \text{ are}$$

$\begin{pmatrix} 1 & 2 & 3 \\ 2 & 3 & 4 \\ 3 & 4 & 5 \end{pmatrix}$

[illegible]

REMARKS: 1.30.041 1.000/
SOUT 00 1. . . 5.5.00

M
A
R
C
H

[illegible]

1017461

Xinli, M.
2011-11-11

1. *Phragmites australis* (Cav.) Trin. ex Steud.

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[illegible]

111 W 111
100 X 100

Received 1991-07-11

Сидорова К.

[illegible]
$$\begin{aligned} & \text{CHOC}_6\text{H}_4\text{SO}_2\text{C}_6\text{H}_4\text{COOH} \\ & \text{S-C}_6\text{H}_4\text{-SO}_2\text{-C}_6\text{H}_4\text{-NH}_2 \end{aligned}$$
[illegible]

ORIGIN

Only Match Most Local Similarity

Mathias 144: Collisionville

1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2808 2809

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[illegible]

100

Figure 1: Schematic representation of the experimental design. The diagram shows a sequence of events: a subject is presented with a stimulus (a word), then a response is given (a word), and finally a feedback is provided (a word). The sequence is repeated for multiple trials. The diagram is divided into two main sections: 'Stimulus' and 'Response'. The 'Stimulus' section shows a sequence of words: 'cat', 'dog', 'bird', 'fish', 'insect', 'mammal', 'reptile', 'amphibian', 'bird', 'fish', 'insect', 'mammal', 'reptile', 'amphibian'. The 'Response' section shows a sequence of words: 'cat', 'dog', 'bird', 'fish', 'insect', 'mammal', 'reptile', 'amphibian', 'bird', 'fish', 'insect', 'mammal', 'reptile', 'amphibian'. The 'Feedback' section shows a sequence of words: 'cat', 'dog', 'bird', 'fish', 'insect', 'mammal', 'reptile', 'amphibian', 'bird', 'fish', 'insect', 'mammal', 'reptile', 'amphibian'. The diagram is labeled 'Figure 1' at the bottom.

11) $\{t, \{ (t, f(t)A^*AAI A I (A I) \}$

$\frac{1}{2}$ $\frac{1}{3}$ $\frac{1}{4}$ $\frac{1}{5}$ $\frac{1}{6}$ $\frac{1}{7}$ $\frac{1}{8}$ $\frac{1}{9}$ $\frac{1}{10}$ $\frac{1}{11}$ $\frac{1}{12}$ $\frac{1}{13}$ $\frac{1}{14}$ $\frac{1}{15}$ $\frac{1}{16}$ $\frac{1}{17}$ $\frac{1}{18}$ $\frac{1}{19}$ $\frac{1}{20}$ $\frac{1}{21}$ $\frac{1}{22}$ $\frac{1}{23}$ $\frac{1}{24}$ $\frac{1}{25}$ $\frac{1}{26}$ $\frac{1}{27}$ $\frac{1}{28}$ $\frac{1}{29}$ $\frac{1}{30}$ $\frac{1}{31}$ $\frac{1}{32}$ $\frac{1}{33}$ $\frac{1}{34}$ $\frac{1}{35}$ $\frac{1}{36}$ $\frac{1}{37}$ $\frac{1}{38}$ $\frac{1}{39}$ $\frac{1}{40}$ $\frac{1}{41}$ $\frac{1}{42}$ $\frac{1}{43}$ $\frac{1}{44}$ $\frac{1}{45}$ $\frac{1}{46}$ $\frac{1}{47}$ $\frac{1}{48}$ $\frac{1}{49}$ $\frac{1}{50}$ $\frac{1}{51}$ $\frac{1}{52}$ $\frac{1}{53}$ $\frac{1}{54}$ $\frac{1}{55}$ $\frac{1}{56}$ $\frac{1}{57}$ $\frac{1}{58}$ $\frac{1}{59}$ $\frac{1}{60}$ $\frac{1}{61}$ $\frac{1}{62}$ $\frac{1}{63}$ $\frac{1}{64}$ $\frac{1}{65}$ $\frac{1}{66}$ $\frac{1}{67}$ $\frac{1}{68}$ $\frac{1}{69}$ $\frac{1}{70}$ $\frac{1}{71}$ $\frac{1}{72}$ $\frac{1}{73}$ $\frac{1}{74}$ $\frac{1}{75}$ $\frac{1}{76}$ $\frac{1}{77}$ $\frac{1}{78}$ $\frac{1}{79}$ $\frac{1}{80}$ $\frac{1}{81}$ $\frac{1}{82}$ $\frac{1}{83}$ $\frac{1}{84}$ $\frac{1}{85}$ $\frac{1}{86}$ $\frac{1}{87}$ $\frac{1}{88}$ $\frac{1}{89}$ $\frac{1}{90}$ $\frac{1}{91}$ $\frac{1}{92}$ $\frac{1}{93}$ $\frac{1}{94}$ $\frac{1}{95}$ $\frac{1}{96}$ $\frac{1}{97}$ $\frac{1}{98}$ $\frac{1}{99}$ $\frac{1}{100}$

100

1

filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

Location/Qualifiers
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ORIGIN

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Best Local Similarity 24.0%; Pred. No. 1.5e-05;

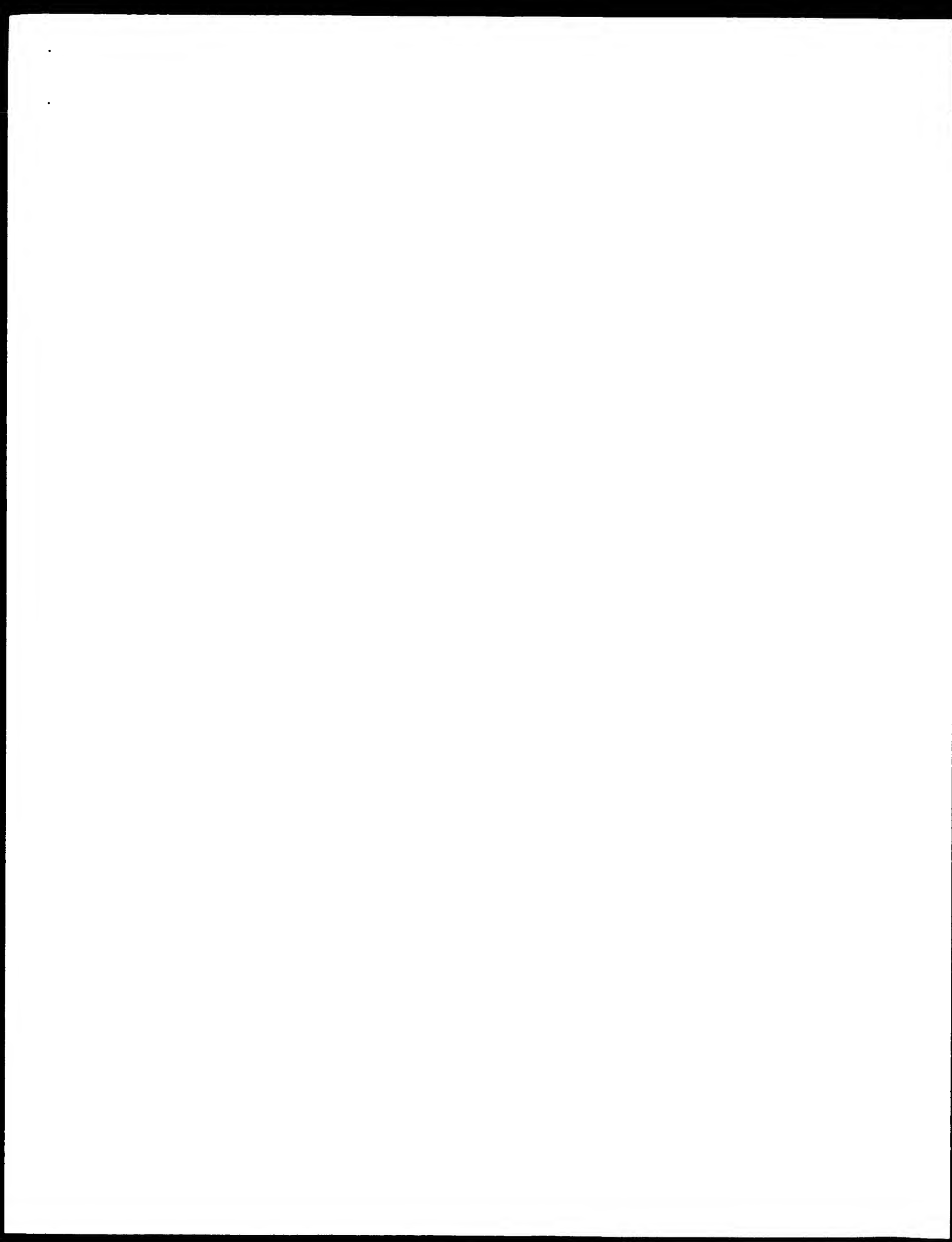
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QY 102 ctgtataacatallaaacollaaaglaaagaalaaagatgaagaaga 161
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QY 222 catgtgtcaaaaacataagagagaaa..... aggaagagagagagataaaga 272
   | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 723 KPIPLWMLALADPLAMHKKKKKPKKKAACCKKCTSPKPRPRPAATWRTIDAMWADAMW 664
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QY 453 aaatlattltaaattlaaagatlgatcattlgaatlaaacaatlaaacaat 512
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Job time: 19093 sec



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Pur on. September 1, 2002, 00:57:11 Search time: 05:59:04
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Title: US-09-678-303-2

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Searched: 383533 seqs, 122816752 residues

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Listing first 45 summaries

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6: /cgn2_6/prodata/1/ina/5D.COMB.seq**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68.2	7.0	19124	2	US-08-487-826B-13
2	66.4	6.8	7218	1	US-08-232-463-14
3	65.8	6.8	837	4	US-08-998-416-288
4	61.8	6.4	615	4	US-08-998-416-186
5	61	6.3	615	4	US-08-998-416-186
6	58.8	6.1	636	4	US-08-998-416-186
7	57.2	5.9	8920	2	US-08-446-855A-1
8	57.2	5.9	8920	2	US-08-446-855A-1
9	54.6	5.6	19124	2	US-08-487-826B-13
10	53.2	5.5	636	4	US-08-998-416-186
11	52	5.4	1511	1	US-07-991-867B-8
12	52	5.4	1511	1	US-08-107-755A-8
13	52	5.4	1511	2	US-08-544-332-8
14	51.8	5.3	837	4	US-08-998-416-288
15	48.8	5.0	658	4	US-08-998-416-595
16	48.2	5.0	6124	4	US-08-213-419B-3
17	48	4.9	2317	1	US-08-749-522-5
18	48	4.9	3974	4	US-08-667-504-3
19	47.6	4.9	863	4	US-08-998-416-498
20	47.2	4.9	6243	2	US-09-056-075-1
21	46.6	4.8	5852	1	US-07-867-106-2
22	46.2	4.8	665	2	US-08-883-795A-36
23	45.8	4.7	5852	1	US-07-867-106-2
24	45.6	4.7	731	1	US-08-451-405A-2
25	45.4	4.7	6768	1	US-08-107-755A-1
26	45.4	4.7	8457	1	US-07-991-867B-1
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28	45	4.6	1186	2	US-08-731-722-5	Sequence 5, Appl 1
29	44.9	4.5	2251	4	US-08-941-677-11	Sequence 11, Appl 1
30	44.7	4.5	4095	4	US-08-941-677-11	Sequence 11, Appl 1
31	44.4	4.6	3528	4	US-08-998-416-288	Sequence 2, Appl 1
32	44.4	4.6	3528	4	US-08-998-416-288	Sequence 2, Appl 1
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34	44.4	4.6	3528	4	US-08-998-416-288	Sequence 2, Appl 1
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38	43.4	4.5	968	4	US-08-122-400B-5	Sequence 5, Appl 1
39	43.4	4.5	968	4	US-08-122-400B-5	Sequence 5, Appl 1
40	43.2	4.4	4383	6	US-08-451-405A-2	Sequence 2, Appl 1
41	42.8	4.4	731	1	US-08-451-405A-2	Sequence 2, Appl 1
42	42.8	4.4	3895	4	US-08-451-405A-2	Sequence 2, Appl 1
43	42.8	4.4	6243	2	US-09-056-075-1	Sequence 1, Appl 1
44	42.8	4.4	8920	2	US-08-446-855A-1	Sequence 1, Appl 1
45	42.8	4.4	8920	2	US-08-446-855A-1	Sequence 1, Appl 1

ALIGNMENTS

RESULT 1
US-08-487-826B-13
Sequence 13, Application US/08487826B
Patent No. 5993827
GENERAL INFORMATION:
APPLICANT: Shim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhan
APPLICANT: Williams, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSER: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: A35
ATTORNEY/AGENT INFORMATION:
NAME: Israelson, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NH121,001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYDROPHOBIC: NO
ANTI-SENSE: NO
US 08 487-826B-13
Query Match 7.0% Score 68.2 DB 2 Length 19124

[illegible]

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D0 5718   gtacaaactataaanaataaatalaagaatgaagtttaantaaatatagaatga 5777
OY    404   aagaatgaatcataagaaatttttgacaaatcatgaabaagaagaatatttt 465
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OY    464   aaacttaaatttgaatcatttgaataacatgtatatttaataattgaagaaga 5873
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RESULT          9
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Sequence 13, Application US/08487B26H
Patent No. 5993827
GENERAL INFORMATION:
APPLICANT: Sim Kim Lo.
APPLICANT: Chinus, Cheban
APPLICANT: Miller, Louis H.
APPLICANT: Patterson, David S.
APPLICANT: Su, Xin Zhang
APPLICANT: Williams, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMIDIOM FALCIPARUM EPITHTROVITE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ACCESSION: GenBank Matrons Wilson & Beazl
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: pc-dos/ms-dos
SOFTWARE: patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: us/08/487,B26H
FILING DATE: 10-sep-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Istaolson, Ned
REGISTRATION NUMBER: 29,655
TELEPHONE/FACSIMILE INFORMATION:
TELEPHONE: (619) 245,8950
TELEFAX: (619) 245,0176
INFORMATION FOR SEQ ID NO.: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,755A
FILING DATE: 19-AUG-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,658
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Salimchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UP114.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1511 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Amsacta macleod entomopoxvirus
FEATURE:
NAME/KEY: CDS
LOCATION: complement (18..218)
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NAME/KEY: CDS
LOCATION: complement (234..782)
FEATURE:
NAME/KEY: CDS
LOCATION: 852..1511
US-08-107-755A-8

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Query Match 5.4%; Score 52; DB 1; Length 1511;
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 Matches 298, Conservative 0, Mismatches 355, Indels 13, Gaps 2.

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DB 615 TAAATATTTTCGTCATGATTTATATTTTATTAATATTAATATTAATATTAATG 674
OY 103 tgtataaacaatataaacaatagaagaatagatgataagagaagagag 162
DB 675 AGTAAATACACATTTTTCATTAATTAATTAATTAATTAATTAATTAATTAATTA 734
OY 163 tgaatattgaacaacatttcttgaacacattga-----gaatatttctg 213
DB 735 TGTGTTTTCGACAGAAACATAGACCAATATTAATTAATTAATTAATTAATTAATTA 794
OY 214 tctcttctctgctgcaaaacacatagagagagagagagagagagagagagag 273
DB 795 TTTGATATATTTTTCAGAAAAAATTAATCAATGAAAAAATTAATTAATTAATTAATG 854
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OY 334 atgagaatattgacaaagctacacaaatagagagagagagagagagagagag 393
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OY 574 aatttgatatttctatataatgagagagagagagagagagagagagagag 633
DB 1155 CCACATTCATAGAAATTTTAAATTCGATCAGTAAATTAATTAATTAATTAAT 1210
OY 634 tagatcaatagaagaataaacgatatataatccctcgaagaaagaaagagat 693
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OY 694 tactaa 699
DB 1271 TATTAAT 1276

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RESULT 13
 US-08-544-332-8
 Sequence 8, Application US/08544332
 Patent No. 5935777
 GENERAL INFORMATION:
 APPLICANT: Meyer, Richard W
 APPLICANT: Hall, Richard L.
 APPLICANT: Guidi, Michael F.
 TITLE OF INVENTION: NO. 5935777-1 Entomopoxvirus Expression System
 NUMBER OF SEQUENCES: 77
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Gerard H. Hencken
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: FL
 COUNTRY: USA
 ZIP: 32606
 COMPUTER PROGRAM: FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1 0, Version #1 25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/544,332
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/991,867
 FILING DATE: 07-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/107,755
 FILING DATE: 19-AUG-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO 92/14818
 FILING DATE: 12-FEB-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/827,685
 FILING DATE: 30-JAN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/657,584
 FILING DATE: 19-FEB-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Hencken, Gerard H.
 REGISTRATION NUMBER: 35,746
 REFERENCE/DOCKET NUMBER: UP114.C4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 904-375-8100
 TELEFAX: 904-372-5800
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1511 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA (genomic)

BASE COUNT	299	3	109	4	210	1
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VERSION	AX105267.1	GI:18921417
KEYWORDS		
SOURCE	synthetic construct.	
ORGANISM	synthetic construct. artificial sequence.	
REFERENCE	1 (bases 1 to 1350).	
AUTHORS	Vezina, L P and H-Aoust M A	
TITLE	Promoter for regulating expression of foreign genes	
JOURNAL	Patent: WO 0125455-A 1 12 APR 2001;	
FEATURES	Medicago Inc. (CA)	
source	location/Qualifiers	
	1..135)	
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DB	309	CAAAAATTGTAAATAATATATTAATAATATTGTAATATTGTAATATTGTAATATTGTA	368		
QY	121	ataagagtttaattgcttaagtaagtaagtaagtaagtaagtaagtaagtaagtaagta	180		
DB	369	AATAAGGGTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	428		
QY	181	gaatttttgcgaagtcataaagaagaagaagaatattttaaataataaagttgaat	240		
DB	429	CAATTTTTCGCCAGTCAATAAAACAAACAAATTAATTTTAAAAATTAAGTTGACT	488		
QY	241	catttgattaaacatgtatatttaataagaattgaagaagttggaataagttgat	300		
DB	489	CATTGATTAAACAGTGAATATTATTAAATGATATGTAAGAAAGCTGGATTAAAGCTGAT	548		
QY	301	tgaatattgaatattggatgaatattgaatattgaatattgaatattgaatattgaat	360		
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DB	729	GATTAACTATTCATTCGTAACGCAATTCATTCGTAACGCAATTCATTCGTAACGCAAT	788		
QY	541	gcaatcctatgagacatctatattatctaaatcaaacattcttccaaagattctgacac	600		
DB	789	GCACCTCTGGCAGACATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	848		
QY	601	caaaaacaaatccacatcttataagccatctctataaaaaatcacacatttgatgtcac	660		
DB	849	CAAAAACCAATCCATCTTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	908		
QY	661	acttgatttccctac	720		
DB	909	ACTTTGATTCCCTTCAACACACATACAAACAGCAAGCAACATTAATTAATTAATTAAT	968		
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Locus					
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ACCESSION	AX036596				
VERSION	AX036596.1		GI:11226191		
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS	Ranco, J., Thomsen, M. and Gruber, V.				
JOURNAL	Patent; FR 2791358 A 2 29 SEP 2000;				
FEATURES	MERISTEM THERAPEUTICS (FR)				
Source	Location/Qualifiers				
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 Matches 326; Conservative 0; Mismatches 206; Indels 3; Gaps 2;

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 Db 506 AGGCAATATATTTCAATGCAATATATATATATATATATATATATATATATATAT 565
 QY 297 gattgaatlaagaatttggatgagatcttcttaaatgagatcttcttctatata 356
 Db 566 TAAATTAATTTTAT 625
 QY 357 tggcagatcttggcagatcttcttaaatgagatcttcttcttcttcttcttctt 416
 Db 626 ATCTTCTGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 685
 QY 417 gatatlaaactcctcaaaaaaaacgatalattacttaaaaaaatcaagcaagta 476
 Db 686 GCAAGTAACTTTTAAAGATATATATTTGATGATTTATATATATATATATATAT 745
 QY 477 gaggatlaaacatgagatcttcttaaatgagatcttcttcttcttcttcttctt 536
 Db 746 GGAAGTAACTTTTAAAGATATATATTTGATGATTTATATATATATATATATAT 805
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RESULT 8
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 LOCUS pea gene for plastocyanin.
 DEFINITION X16082.1 Cl:20845
 ACCESSION X16082.1 Cl:20845
 VERSION
 KEYWORDS electron carrier; photosynthesis; plastocyanin.
 SOURCE pea.
 ORGANISM Pisum sativum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids 1; Fabales; Fabaceae; Papilionoideae; Viciae;
 Pisum.

REFERENCE 1 (bases 1 to 1505)
 AUTHORS Last,D.I. and Gray,J.C.
 TITLE Plastocyanin is encoded by a single-copy gene in the pea haploid genome
 JOURNAL Plant Mol Biol 12, 655-666 (1989)
 FEATURES location/Qualifiers
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 BASE COUNT 460 a 299 c 283 g 463 t
 ORIGIN

Query Match 24.5%; Score 179.4; DB R; Length 1505;
 Best Local Similarity 60.9%; Pred. No. 3,3e+20;
 Matches 326; Conservative 0; Mismatches 206; Indels 3; Gaps 2;

QY 177 tagagatttttggcagatcattataaagaagaataatcttcttaaatlaaagaatt 236
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 QY 237 gactcatttgaatlaaacatgagatcttcttaaatgagaaagattgagataaagt 296
 Db 326 AGGCAATATATTTCAATGCAATATATATATATATATATATATATATATATATAT 385
 QY 297 gattgaatlaagaatttggatgagatcttcttaaatgagatcttcttctatata 356
 Db 386 TAAATTAATTTTAT 445
 QY 357 tggcagatcttggcagatcttcttaaatgagatcttcttcttcttcttcttctt 416
 Db 446 ATCTTCTGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 505
 QY 417 gatatlaaactcctcaaaaaaaacgatalattacttaaaaaaatcaagcaagta 476
 Db 506 GCAAGTAACTTTTAAAGATATATTTGATGATTTATATATATATATATATATATAT 565
 QY 477 gaggatlaaacatgagatcttcttaaatgagatcttcttcttcttcttcttctt 536
 Db 566 GGAAGTAACTTTTAAAGATATATTTGATGATTTATATATATATATATATATATAT 625

LOCUS	AX036601	280 bp	linear	Mar 16-Nov-2000
DEFINITION	Sequence 7 from Patent FR2791358.			
ACCESSION	AX036601			
VERSION	AX036601.1	GI:1226196		
KEYWORDS				
SOURCE				
ORGANISM	synthetic construct. artificial sequence.			
REFERENCE	1 (bases 1 to 280) Rance, I., Theisen, M. and Gruber, V. Patent: FR 2791358-A 7-29-SEP-2000; MERRISTEM THERAPEUTICS (FR)			
AUTHORS				
JOURNAL				
FEATURES	location/Qualifiers			
source	1..280			
	/organism="synthetic construct"			
	/db_xref="taxon:32630"			
promoter	1..280			
	/note="The promoter MPr110 was created by inserting at position -99 bp of MPr1098 an element of 18 bp containing a 'G' box and by fusing a sequence of 44 bp of the RNA 35S Camv promoter			
	promoter MPr110"			
BASIS COUNT	88 a 73 c 42 g 77 t			
ORIGIN				
Query Match	12 2% Score 89; Dh 6; Length 280;			
Best Local Similarity	76 2% Prod No 21-05;			
Matches 144:	Conservative 0; Mismatches 25; Indels 20; Gaps 27			
QY	542 cactctgtgacacatcatatcttaaatc----- acacactctt 582			
Db				
68 CACCTCTGTGGCCACATCAATATATATGAAATCAAGCCAGAGCGAGAACATATCTT 127				
QY	583 ccacacatctggccacacacacacacacacatccatccacatcttatcaccctctctataacaa 641			
Db				
128 CCACACATCTTGGCCACACACACACACACACATCCATCTTATCATCTTATATAAAAA 187				
QY	642 tcaacactgttagctagactatcttattccctctcaacacacacacacacacacacacacacac 701			
Db				
188 TCACCTCTGTGTTGTCTCTCTTTCATTTCCTTTAAACATATATATAAACTCATATATAAA; 247				
QY	702 ttaattaat 710			
Db				
248 AAACCTCATTT 256				
RESULT 13				
LOCUS	AX036603	290 bp	linear	Mar 16-Nov-2000
DEFINITION	Sequence 9 from Patent FR2791358.			
ACCESSION	AX036603			
VERSION	AX036603.1	GI:1226198		
KEYWORDS				
SOURCE				
ORGANISM	synthetic construct. artificial construct. artificial sequence.			
REFERENCE	1 (bases 1 to 296) Rance, I., Theisen, M. and Gruber, V. Patent: FR 2791358-A 9-29-SEP-2000; MERRISTEM THERAPEUTICS (FR)			
AUTHORS				
JOURNAL				
FEATURES	location/Qualifiers			
source	1..296			
	/organism="synthetic construct"			
	/db_xref="taxon:32630"			
promoter	1..296			
	/note="Promoter MPr111 created by inserting at -99 bp position of MPr1098, an 18 bp element containing a 'G' box and fusing a sequence of 58 bp (duplication of the element as2 and as1)			
	promoter MPr111"			

BASE COUNT	94 a	74 c	45 g	83 t		
ORIGIN						
Query Match	12.2%, Score 89, 148 b, length 270					
Best Local Similarity	76.2%, Pred. No. 2, 1e-05;					
Matches 144;	Conservative 0; Mismatches 25; Indels 20; Gaps 2;					
OY	542	cactctgtggtacatctatctaatc-----	aacatctctt	582		
DB	84	CACCTGTGTGGCCACATCTATCTAATTAATCTAAAGCCACGTCGGACGATAAACATATCTT	11111111	143		
OY	583	ccacacatctaaagccacacaaaaa ccaatccacatcttatacccatctataaaaaa	641			
DB	144	CCACACATCTTAAGCCACACAAAAAACCCCAATCCACATCTTATATACATTCATTAATAAAAAA	203			
OY	642	tcaacatctgtgtgtctaacatcttgaattcccttcaaacacatacaagaagaactaa	701			
DB	204	TCACTTGTGTGTGTCTCTTTTCATTTCTTTCAATTCCTTTCAAAATATATATATATATAT	263			
OY	702	ttaattaat	710			
DB	264	AAACTCATTT	272			
RESULT 14						
AX036602						
LOCUS	AX036602	383 bp	DNA	14 Nov 2000		
DEFINITION	Sequence from Patient PR2791358.					
ACCESSION	AX036602					
VERSION	AX036602.1	GI:1126197				
KEYWORDS						
SOURCE	synthetic construct.					
ORGANISM	synthetic construct.					
REFERENCE	1 (bases 1 to 303)					
AUTHORS	Rance, I., Theisen, M. and Gruber, V.					
JOURNAL	Patent: EP 2,791,358-A 8 29-SEP-2000;					
FEATURES	MERISTEM THERAPEUTICS (PT)					
source	location/Qualifiers					
	1..303					
	/organism="synthetic construct"					
	/db_xref="taxon:4650"					
promoter	1..303					
	/note="The promoter Mpr1153 was obtained by fusing a					
	sequence of 78 bp of the promoter pef1, stretching from					
	position -582 to position -510 bp modified by adjunction					
	of a 'g box					
	promoter Mpr1153"					
BASE COUNT	101 a	78 c	41 g	83 t		
ORIGIN						
Query Match	12.2%, Score 89, DB 6; Length 303;					
Best Local Similarity	76.2%, Pred. No. 2, 1e-05;					
Matches 144;	Conservative 0; Mismatches 25; Indels 20; Gaps 2;					
OY	542	cactctgtggtacatctatctaatc-----	aacatctctt	582		
DB	91	CACCTGTGTGGCCACATCTATCTAATTAATCTAAAGCCACGTCGGACGATAAACATATCTT	11111111	150		
OY	583	ccacacatctaaagccacacaaaaa ccaatccacatcttatacccatctataaaaaa	641			
DB	151	CCACACATCTTAAGCCACACAAAAAACCCCAATCCACATCTTATATACATTCATTAATAAAAAA	210			
OY	642	tcaacatctgtgtgtctaacatcttgaattcccttcaaacacatacaagaagaactaa	701			
DB	211	TCACTTGTGTGTGTCTCTTTTCATTTCTTTCAATTCCTTTCAAAATATATATATATATAT	270			
OY	702	ttaattaat	710			
DB	271	AAACTCATTT	279			


```

OY 421 attatccctcccaaaaaaacggtattacttaaaaaatctaaagccagctagag 480
    |||||||
Db 661 attatccctcccaaaaaaacggtattacttaaaaaatctaaagccagctagag 720
OY 481 gataaatccatcccaaccatccacacatccctgataagataaacctttaagccac 540
    |||||||
Db 721 gataaatccatcccaaccatccacacatccctgataagataaacctttaagccac 780
OY 541 gacactctgagacatctcattatctaaatcagacatcttctgagacacacac 600
    |||||||
Db 781 gacactctgagacatctcattatctaaatcagacatcttctgagacacacac 840
OY 601 caaaaacccatccatcttcttaacacacatcttcttaacacacacatcttcttaac 660
    |||||||
Db 841 caaaaacccatccatcttcttaacacacatcttcttaacacacacatcttcttaac 900
OY 661 acttgatccctcccaacacacacacacacacacacacacacacacacacacac 720
    |||||||
Db 901 acttgatccctcccaacacacacacacacacacacacacacacacacacacac 960
OY 721 gagaagaatg 731
    |||||||
Db 961 gagaagaatg 971

```

RESULT 3

AA52126
ID AA502126 standard; DNA: 1350 bp

XX AAS02126;

XX 18-JUL-2001 (first entry)

XX Promoter #1 for regulating expression of foreign genes

XX Promoter; transgenic plant; monocotyledon, dicotyledon, gymnosperm; ds.

XX Synthetic.

XX W0200125455.A2.

XX 12-APR-2001.

XX 02-OCT-2000. 2003W01A01144

XX 04-OCT-1999; 99QS-0157129

XX (MED1-) MNP1CAGG INC

XX Vezina L, D'Aoust M;

XX MPI; 2001-46631b/27.

XX Novel promoter for regulating expression of foreign genes in transgenic

XX plants -

XX Claim 1; Page 8; 9pp; English.

XX The sequence represents the coding sequence of promoter #1 for regulating
XX expression of foreign genes in transgenic organisms. The promoter is
XX useful for regulating the expression of foreign genes in transgenic
XX organisms, particularly plants, e.g. monocotyledons, dicotyledons or
XX gymnosperms, by preparing a transgenic organism using an expression
XX construct comprising the promoter and an open reading frame (ORF) of a
XX gene.

XX Sequence 1350 bp; 482 A; 236 C; 230 G; 402 T; 0 other.

Query Match 100.0%; Score 731; DB 22; Length 1350;
Test local similarity 100.0%; Pred No 6 8c-133;

```

Matches 731; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 aagaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaa 60
    |||||||
Db 249 aagaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaa 308
OY 61 caaaagttgucacaaatcagttgacaaatcagttgacaaatcagttgacaaatcagttgac 120
    |||||||
Db 309 caaaagttgucacaaatcagttgacaaatcagttgacaaatcagttgacaaatcagttgac 368
OY 121 aataagaaatcagttgacaaatcagttgacaaatcagttgacaaatcagttgacaaatc 180
    |||||||
Db 369 aataagaaatcagttgacaaatcagttgacaaatcagttgacaaatcagttgacaaatc 428
OY 141 gaaatcttggagaaatcagttgacaaatcagttgacaaatcagttgacaaatcagttgac 240
    |||||||
Db 429 gaaatcttggagaaatcagttgacaaatcagttgacaaatcagttgacaaatcagttgac 488
OY 241 cattgatcaacatcagttgacaaatcagttgacaaatcagttgacaaatcagttgacaaat 300
    |||||||
Db 489 cattgatcaacatcagttgacaaatcagttgacaaatcagttgacaaatcagttgacaaat 548
OY 301 taatgaatgaatcagttgacaaatcagttgacaaatcagttgacaaatcagttgacaaat 360
    |||||||
Db 549 taatgaatgaatcagttgacaaatcagttgacaaatcagttgacaaatcagttgacaaat 608
OY 361 ccaataagacatcagttgacaaatcagttgacaaatcagttgacaaatcagttgacaaat 420
    |||||||
Db 609 ccaataagacatcagttgacaaatcagttgacaaatcagttgacaaatcagttgacaaat 668
OY 421 attatccctcccaaaaaaacggtattacttaaaaaatctaaagccagctagag 480
    |||||||
Db 669 attatccctcccaaaaaaacggtattacttaaaaaatctaaagccagctagag 720
OY 481 gataaatccatcccaaccatccacacatccctgataagataaacctttaagccac 540
    |||||||
Db 729 gataaatccatcccaaccatccacacatccctgataagataaacctttaagccac 788
OY 541 gacactctgagacatctcattatctaaatcagacatcttctgagacacacacacacacac 600
    |||||||
Db 789 gacactctgagacatctcattatctaaatcagacatcttctgagacacacacacacacac 848
OY 601 caaaaacccatccatcttcttaacacacatcttcttaacacacacatcttcttaacacacac 660
    |||||||
Db 849 caaaaacccatccatcttcttaacacacatcttcttaacacacacatcttcttaacacacac 908
OY 661 acttgatccctcccaacacacacacacacacacacacacacacacacacacacacacacac 720
    |||||||
Db 909 acttgatccctcccaacacacacacacacacacacacacacacacacacacacacacacac 968
OY 721 gagaagaatg 731
    |||||||
Db 969 gagaagaatg 979

```

RESULT 4

AAA96458
ID AAA96458 standard; DNA: 623 bp.

XX AAA96458;

XX 08-FEB-2001 (first entry)

XX Nucleotide sequence of the promoter MPT1097.

XX put promoter; chimeric promoter; transgenic plant; MPT1097;

XX plastocyanin gene promoter; ss.

XX Synthetic.

XX Pisum sativum.
XX W020005690b-A1.

Search completed: Sep 03 04:04:22
Job: 1 time: 00:04:00

organism: "Medicago truncatula"
db_xref: "taxon:3880"
colone: "N0502101"
clone: "1b-E" *erecting flower*
tissue: "developing flowers"
development: "early stage"
very young: "developing, fully opened flowers and flowers in early transition into pods"

BASE COUNT	170.4	147.5	119.9	174.1	others
ORIGIN					

Matchos	11.2	Conservatio	0	Mismatches	6	Indels	3	Gaps	1
best local similarity	42.06	47.00	44.40	40.72					

648 *****707

[illegible]

708	a	708
b	1	121

REF: 11,7

FACTORS	683 bp	mtDNA	EST 19-DEC-2000
DEFINITION	MF677150		
	MF047A021P1P1006	low-voltage local Medicago	truncatula cDNA clone
	MF047A021F 1-2	mtDNA	sequenced

```

VERSION      13F647150.1      01:11'001.00H
KEYWORDS     EST
SOURCE       bacterial modio

```

ORGANISM
Moderate to abundant
Eukaryotic: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta
Spermatophytes: Magnoliopsida: eudicotyledons: Core eudicots:

REFERENCE
1 (bases 1 to 4)
LITTON, J. O. J. and WATTS, A. D. "Correlation of
Alcohols

Expressed Sequence Tags from the Salmonellosis Nucleic Acid Database
Medicago truncatula cDNA library

COMMENT
Contact: May 60
Plant Biology Institute
The Samuel Roberts Noble Foundation

Tel: 580 221 7391
Fax: 580 221 7380

Insert length: 604 Std Error: 0.00
Plate: 04 / Row: A Column: 02
Spot Element: $\text{Co}^{57}\text{Fe}^{59}\text{Ni}^{60}\text{Cu}^{64}\text{Zn}^{66}\text{Ga}^{67}\text{Ge}^{70}\text{As}^{73}\text{Se}^{76}\text{Br}^{78}\text{Kr}^{81}\text{Rb}^{85}\text{Sr}^{87}\text{Y}^{89}\text{Zr}^{90}\text{Tc}^{99}\text{Mo}^{99}\text{Ru}^{100}\text{Rh}^{101}\text{Pd}^{102}\text{Ag}^{107}\text{Cd}^{111}\text{In}^{113}\text{Sn}^{115}\text{Sb}^{121}\text{Te}^{127}\text{I}^{127}\text{Xe}^{131}\text{Ba}^{135}\text{La}^{138}\text{Ce}^{140}\text{Pr}^{141}\text{Nd}^{143}\text{Pm}^{147}\text{Sm}^{150}\text{Eu}^{151}\text{Gd}^{155}\text{Tb}^{158}\text{Dy}^{162}\text{Ho}^{164}\text{Er}^{167}\text{Tm}^{168}\text{Yb}^{172}\text{Lu}^{174}\text{Hf}^{178}\text{Ta}^{180}\text{W}^{182}\text{Re}^{185}\text{Os}^{187}\text{Ir}^{191}\text{Pt}^{194}\text{Au}^{196}\text{Hg}^{198}\text{Th}^{230}\text{Pa}^{231}\text{U}^{233}\text{Np}^{235}\text{Pu}^{238}\text{Am}^{241}\text{Cm}^{244}\text{Bk}^{246}\text{Cf}^{249}\text{Es}^{252}\text{Fm}^{254}\text{Md}^{257}\text{No}^{259}\text{Lw}^{261}\text{Ac}^{227}\text{Th}^{229}\text{Pa}^{233}\text{U}^{235}\text{Np}^{237}\text{Pu}^{239}\text{Am}^{243}\text{Cm}^{245}\text{Bk}^{247}\text{Cf}^{249}\text{Es}^{251}\text{Fm}^{253}\text{Md}^{255}\text{No}^{257}\text{Lw}^{259}\text{Ac}^{225}\text{Th}^{227}\text{Pa}^{229}\text{U}^{231}\text{Np}^{233}\text{Pu}^{235}\text{Am}^{237}\text{Cm}^{239}\text{Bk}^{241}\text{Cf}^{243}\text{Es}^{245}\text{Fm}^{247}\text{Md}^{249}\text{No}^{251}\text{Lw}^{253}\text{Ac}^{223}\text{Th}^{225}\text{Pa}^{227}\text{U}^{229}\text{Np}^{231}\text{Pu}^{233}\text{Am}^{235}\text{Cm}^{237}\text{Bk}^{239}\text{Cf}^{241}\text{Es}^{243}\text{Fm}^{245}\text{Md}^{247}\text{No}^{249}\text{Lw}^{251}$

FEATURES
SOURCE
1. 684
/orquid.com "Medicine" (Fruitful) a "n

colonne "NE047AD21.1"
/colonne 1 to "developing local"
/colonne 1 vers "local"

young in the forest, growing in a
"dark, wet, shaded spot, radiating a mild odor of
young, above, pink, mature and senescent leaves."

Query Match: 11.78; Score: 85.8; Pk 1st; Length: 688;

	Matches	Corrective	Mismatch	Pairs	Gaps
	1067	190	127	1008	11
Total	1267	190	127	1008	11

[illegible]

61 TTGAGATGCTACCTCTTGATTCCTTCATACACATAGAAACATACATATATTAATTAATCTCT

UD	1.21	A	1.21
UD	1.21	A	1.21

[illegible]

VERSION	13145756.1	0111440804
KEYWORDS		
SOURCE	barrel medic,	

Fukuyama, Y. Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicotyledons: rosids.

REFERENCE	Medicato: I (basos I to 63)
AUTHORS	Liu, J., Scott, A. D., Harris, A. R., Gonzales, R. A., Holler, J., Flores

TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula phosphate-starved leaf library

CONTACT: HARRISON M.
PLANT BIOLOGY DIVISION
THE SAMUEL ROBERTS NOBLE FOUNDATION

Tel: 5800 221 7425
Fax: 5800 221 7480
Email: miba@riscan.mobi.com

```

insert length: 64      seq error: 0.00
plate: 105    row: 7    column: 07
seq primer:  (5'-ATTAAGGAAATAC-3')ATGTA-

```

SOURCE
1. 687
/corruptionⁿ
Medicine + corruptionⁿ
de vrotⁿ + corruptioⁿ

```

/colono.lib "phosphate starved leaf"
/issue type "leaf"

```

For the "Vector" *Lambdula Zett.* trineural plants were not and grown for a further

periods, the plants were fertilized three times with 1/2 Hoagland's solution containing only 300 mg potassium phosphate. RNA was prepared from leaves ground in liquid

Very bad	1.76	0.0000	0.97
Fair	0.00	0.0000	0.97
Post local similarity	91.98%	Pred. No. 0.000172	
Mutual loss	0.000000	Misclassified	0.000000
			0.000000

601 CAGGACCGCCTCCGCATCTTT dTGGGCAATTCTdGAGGAATCCGCGCTTGtGTGATcAGC.

LOCUS	Drosophila	1101 bp	DNA	linear	GSS 03-JUN-1998
DEFINITION	Drosophila melanogaster genome survey sequence. HITS end of BAC # BAR05N11 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.				
ACCESSION	AL061936				
VERSION	AL061936.1 GI:4940214				
KEYWORDS	GSS.				
SOURCE	fruit fly.				
ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 1101)				
REFERENCE	Direct Submission				
AUTHORS	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : seipet@genoscope.cns.fr)				
TITLE	Web : www.genoscope.cns.fr				
JOURNAL	determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org. The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osuwawa and Aaron Mamosser at Peter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI 98 and was constructed by partial EcoRI digestion of Drosophila RNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the HACBAC Resource Center can be found at http://carpac.med.buffalo.edu/drosophila_bac.htm.				
FEATURES	Location/Qualifiers				
SOURCE	1..1101 /organism="Drosophila melanogaster" /db_xref="taxon:7227" /clone_lib="RPCI-98" /clone="BACR05N11" /note="end : TE13"				
BASE COUNT	631 a 7 c 28 g 289 t 146 others				
ORIGIN					
Query Match	9.8%; Score 72; DR 12; Length 1101;				
Best Local Similarity	43.6%; Pred. No. 0.02;				
Matches 198; Conservative 21; Mismatches 235; Intels 0; Gaps 0;					
OY	1 agaggaagaagaagagagagagatacaaaactaatgtgagtatgagagagaagtgtga 60				
DB	258 AA 317				
OY	61 caaaqtlgtaccaaatlgtlgaacaatatcatlgaqaatlga'aaagctlacaa 120				
DB	318 CAAAAAATAA 377				
OY	121 aataagqatlaatlgtcgttaataataaagatgacgcattagaagaalgtacca 180				
DB	378 AA 437				
OY	181 gaatttcggcaagtcataaagaagaagaataatttcttaaataaagt-gagt 240				
DB	438 AA 497				
OY	241 calligaltaaacatlgattlattaatgaatlgaagaagatllgaagt-gtat 300				
DB	498 AAAAAAAAAAAAAAAAAAAATTAATTATTTTWTATAATTATTTTWTATTTTTCF 557				
OY	301 taagtaataaatltgucgtcaaatltaatlgaacatllgatclttccatata-tgcc 360				
DB	558 TWTATATTTTATTTTTTAAMWMAAATTTAATAAAAMWMTTATTTTATATWTAAMWA 617				
OY	361 ccataagagcgactaact-attcttatattcatagatcaataaagaagaataaaagtgat 420				

D0 618 AAAAAAAAAATTAAAWWTTTTTTWTAAIAIAIAAAAAAAAAATMAAWTWIIIA 677

Oy 421 attaatccctcccaaaaaaaacgataatt 454

D0 678 TTTTATTAATTTAAATTTTAAAAWTTTWTATT 711

Search completed: August 31, 2002, 23:46:55
Job time: 19101 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 2, 2002, 00:57:51 : Search time 96.05 seconds
(without alignments)
1869.423 Million cell updates/sec

Title: US-09-678-303-3

Perfect score: 731
Sequence: 1 agagagaagaagaagaagggg dated 01/14/2002 731

Scoring table: IDENTITY NUC Gapout 1 0
Gapin 10 0 Gapout 1 0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Issued_Patents_NA:

- 1: /cgn2_6/pdata/1/ina/5A.COMB.seq*
- 2: /cgn2_6/pdata/1/ina/5B.COMB.seq*
- 3: /cgn2_6/pdata/1/ina/5C.COMB.seq*
- 4: /cgn2_6/pdata/1/ina/5D.COMB.seq*
- 5: /cgn2_6/pdata/1/ina/5E.COMB.seq*
- 6: /cgn2_6/pdata/1/ina/5F.COMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	61	8.3	7218	1	Sequence 14, Appl
2	48	6.6	2317	3	Sequence 5, Appl
3	48	6.6	3974	4	Sequence 3, Appl
4	47.4	6.5	837	4	Sequence 288, Appl
5	46	6.3	19124	2	Sequence 13, Appl
6	45.8	6.3	5852	1	Sequence 2, Appl
7	45.4	6.2	6768	1	Sequence 1, Appl
8	45.4	6.2	8457	2	Sequence 1, Appl
9	45.4	6.2	8457	2	Sequence 1, Appl
10	45	6.2	19124	2	Sequence 13, Appl
11	44.8	6.1	847	4	Sequence 288, Appl
12	44.6	6.1	2251	4	Sequence 13, Appl
13	44.6	6.1	3095	6	Sequence 13, Appl
14	44.4	6.1	615	4	Sequence 13, Appl
15	44.2	6.0	8920	2	Sequence 1, Appl
16	44.2	6.0	8920	2	Sequence 1, Appl
17	43.6	6.0	3450	4	Sequence 1, Appl
18	43.4	5.9	740	4	Sequence 1, Appl
19	43.4	5.9	6243	2	Sequence 1, Appl
20	42.8	5.9	8920	4	Sequence 1, Appl
21	42.8	5.9	8920	4	Sequence 1, Appl
22	42.2	5.8	15231	3	Sequence 1, Appl
23	42.2	5.8	176373	3	Sequence 1, Appl
24	42	5.7	863	4	Sequence 1, Appl
25	41.8	5.7	3618	1	Sequence 1, Appl
26	41.6	5.7	6124	4	Sequence 1, Appl
27	41.6	5.7	7653	3	Sequence 1, Appl

28	41.6	5.7	7653	3	US-08-368-704C-1
29	41.6	5.7	7653	5	PCT-US93-05701 18
30	41.6	5.7	7653	5	PCT-US93-05701 18
31	41.4	5.7	1441	4	US-08-821-994-63
32	41.2	5.6	7653	2	US-08-394-1898-1
33	41	5.6	8454	4	US-08-998-416-405
34	41	5.6	1450	3	US-08-617-860B-22
35	40.8	5.6	6584	4	US-08-998-416-565
36	40.8	5.6	5852	1	US-07-867-106-2
37	40.6	5.6	662	4	US-08-998-416-185
38	40.6	5.6	662	4	US-08-998-416-191
39	40.6	5.6	665	4	US-08-998-416-417
40	40.6	5.6	701	4	US-08-998-416-701
41	40.6	5.6	711	4	US-08-998-416-785
42	40.6	5.6	724	4	US-08-998-416-785
43	40.6	5.6	732	4	US-08-998-416-1036
44	40.6	5.6	767	4	US-08-998-416-172
45	40.6	5.6	827	4	US-08-998-416-535

ALIGNMENTS

RESULT 1
US-08-232-463-14/C
Sequence 14, Applicant US/08222463
Patent No. 5670367

GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHUEFLINGER, F.
TITLE OF INVENTION: PEROXIMANT FOWLEPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESS: Policy & Partner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08-232-463
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08222463
FILING DATE:
APPLICATION NUMBER: 08/21/99
FILING DATE: 08/21/99

ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
FIRM/INVENTOR NAME: 08/21/99
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ19-F15
US-08-232-463-14

Sequence 1, Appl
Sequence 18, Appl
Sequence 1, Appl
Sequence 6, Appl
Sequence 1, Appl
Sequence 405, Appl
Sequence 22, Appl
Sequence 595, Appl
Sequence 2, Appl
Sequence 185, Appl
Sequence 191, Appl
Sequence 917, Appl
Sequence 701, Appl
Sequence 785, Appl
Sequence 683, Appl
Sequence 1036, Appl
Sequence 472, Appl
Sequence 535, Appl

Query Match	0.38; Score 61; PB 1; Length 2216;
Best Local Similarity	7.5%; P-Ped. No. 6, 40 (5);
Matches	31; Conservative 166; Indels 0

[illegible]

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Query Match	6.5%	Score 48	DB 4	Length 2417
Post-Clust Similarity	50.4%	Prod. No.	0.033	
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				Gaps 12

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1      RESULT1
2      US-08-467 504 4/c
3      Sequence 3, Application US/08467504
4      Patent No. 6211410
5      GENERAL INFORMATION:
6      APPLICANT : John, Malyakal E.
7      TITLE OF INVENTION: FLUKE THE MOTHER
8      NUMBER OF SEQUENCES: 16
9      CORRESPONDENT ADDRESS:
10     ADDRESS: Quail's & Featy
11     STREET: 411 East Wisconsin Avenue
12     CITY: Milwaukee
13     STATE: WI
14     COUNTRY: U.S.A.
15     ZIP: 53202 4497
16     COMPUTER AVAILABLE FROM:
17     MEDIUM TYPE: Floppy disk
18     COMPUTER: IBM PC compatible
19     OPERATING SYSTEM: PC DOS/MS DOS
20     SOFTWARE: PATENT IN PROGRESS #1.0, Version #1.0
21     CURRENT APPLICATION DATA:
22     APPLICATION NUMBER: 09/267467, 504
23     FILING DATE:
24     CLASSIFICATION: 800
25     ATTORNEY/AGENT INFORMATION:
26     NAME: Baker, John C.
27     REGISTRATION NUMBER: 45,414
28     REFERENCE/PRIORIT NUMBER: 110229, 91152
29     TELECOMMUNICATION INFORMATION:
30     TELEPHONE: (414) 277-6709
31     TELEFAX: (414) 271-4562
32     INFORMATION FOR SEQ ID NO: 4:
33     SEQUENCE CHARACTERISTICS:
34     LENGTH: 4974 base pairs
35     TYPE: nucleic acid
36     STRANDEDNESS: double
37     topology: linear
38     MAPPING TYPE: DNA (genomic)
39     OS-08 467 504 4

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Query Match	Similarity	Score	Pos	Length
Host Local	50.4%	Prod. No.	0.046	
Matches	14%	Conservative	14%	100%
159	11	11	11	11

NAME: Bennett, Gerald H.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: UP114,074
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
FAX: 904-375-6000

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; INFORMATION FOR SEQ ID NO: 1:
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; SOURCE: UNPUBLISHED

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LENGTH: 8457 base pairs
TYPE: nucleic acid

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STRANDNESS: double
Topology: unknown
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MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:

ACKNOWLEDGMENTS

LOCATIONS: (65. . 1459)

NAME/KEY: CDS

FEATURES

LOCATION: complement (22.49 - 24.75)
FEATURE:

NAME/KEY:	CDS
LOCATION:	REF 09487

NAME/KEY : CUS
FLATIDIR :

LOCALION: 3080, 6091
FEATURE:

COMPLEMENT (4.277 - 4.768)

Query Match: 6.28; Score: 4

Matches 156; Conservative 0; Miss

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Idb 2254 CAAAAAATAAGACTGTAAATGAT

by the appropriate individual.

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1955 GATTACATTAATCACT 1933

RESOL 10
US-08-487-826B-13/c

Patent No. 5993827

APPLICANT: Sim, Kim L.

APPLICANT: Miller, Louis H.

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100

GenCore version 4.5
Copyright (c) 1993 2000 CompuGen Ltd

OM nucleic - nucleic search, using sw model

Run on: August 31, 2002, 23:46:03 : Search time 412.93 seconds
(without alignments)
6868.783 Million cell updates/sec

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scoring table: `UNIGO_NOC`
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Searched: 1797656 seqs, 10463268293 residues

WORD SIZE : 0

Total number of hits satisfying chosen parameters:

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Maximum DB seq length: 2000000000
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Post-processing: listing first 45 summaries

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32:	em.hlg.other:	*
33:	em.hlg.in:	*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Query Score	Match Length	DR	ID	Description
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1	1350	106.0	1360	6	AX105627	AX105627 Sequence
2	971	71.9	971	6	AX105628	AX105628 Sequence
3	731	54.1	731	6	AX105629	AX105629 Sequence
4	4	4.2	4.5	6	AX036537	AX036537 Sequence
5	57	4.2	5.3	6	AX036536	AX036536 Sequence
6	6	4.2	8.4	6	AX036535	AX036535 Sequence
7	57	4.2	9.98	6	PSPEP	PSPEP Sequence
8	57	4.2	15.05	8	ESPLAS	ESPLAS Sequence
9	34	2.5	68	6	AX036607	AX036607 Sequence
10	34	2.5	7.93	6	AX036600	AX036600 Sequence
11	32	2.4	2.07	6	AX036598	AX036598 Sequence
12	31	2.3	2.86	6	AX036601	AX036601 Sequence
13	31	2.3	2.6	6	AX036603	AX036603 Sequence
14	31	2.3	3.93	6	AX036602	AX036602 Sequence
15	27	2.0	7.2	6	AX036609	AX036609 Sequence
16	27	2.0	2.65	6	AE2982	AE2982 Sequence
17	25	1.9	2.20	6	AX036604	AX036604 Sequence
18	25	1.9	2.9	6	AX036616	AX036616 Sequence
19	25	1.9	1.76	8	ALPHNYT	ALPHNYT Sequence
20	24	1.9	1.715	8	MS018296	MS018296 Medicago sa
21	24	1.8	1.043	3	AX031455	AX031455 Lepocora
22	24	1.8	6.6957	2	AC083979	AC083979 Homo sapi
23	24	1.8	16.648	10	AC073469	AC073469 Homo sapi
24	24	1.8	16.918	9	AC104185	AC104185 Homo sapi
25	24	1.8	16.6381	39	AC021208	AC021208 Homo sapi
26	24	1.8	16.7918	2	AC104188	AC104188 Homo sapi
27	24	1.8	21.8126	2	AE27083	AE27083 Mus muscu
28	23	1.7	2.81	6	AX036599	AX036599 Sequence
29	23	1.7	5.219	6	AX345174	AX345174 Sequence
30	23	1.7	7.777	3	AE93325	AE93325 Sequence
31	23	1.7	3.8666	8	SPAC2349	SPAC2349 Sequence
32	23	1.7	13.4195	1	SYSLR	SYSLR Sequence
33	23	1.7	2.65985	6	AC087226	AC087226 Mus muscu
34	23	1.7	3.49980	6	AX344557	AX344557 Sequence
35	23	1.6	1.732	2	AX038242	AX038242 Gryza sat
36	22	1.6	3.3751	2	AC099966	AC099966 Mus muscu
37	22	1.6	9.596	6	AL550487	AL550487 Human DNA
38	22	1.6	11.7841	2	AG154285	AG154285 Gryza sat
39	22	1.6	13.9894	2	AC104711	AC104711 Gryza sat
40	22	1.6	13.9423	8	AC088755	AC088755 Gryza sat
41	22	1.6	14.9931	4	AC032243	AC032243 Homo sapi
42	22	1.6	15.030	9	AL157932	AL157932 Homo DNA
43	22	1.6	16.0404	9	AL159152	AL159152 Homo DNA
44	22	1.6	161.927	2	AC084818	AC084818 Gryza sat
45	22	1.6	167.931	2	AC093462	AC093462 Homo cyn

ALIGNMENTS

RESULT	1
AXI05267	
LOCUS	350 bp
DEFINITION	inA
Sequence 1 from Patent WO0225455.	1998 Apr - 2001

VERSION AX105267.1 GI:13921417

ORGANISM

REFERENCE

2011

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Source

BRUCE MCDONALD
ORIGIN

[illegible]

RESULT	3			
AXI05269				
LOCUS	AXI05269	731 bp	DNA	linear PAT 40-APR-2001
DEFINITION	Sequence 3 from Patent WO0125455.			
ACCESSION	AXI05269			
VERSION	AXI05269.1	GI:13921419		
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
COUNCIL				
FEATURES				
SOURCE				

```

        synthetic construct.
        synthetic construct.
        artificial sequence.
        1 (bases 1 to 731)
        Vezina,L.P. and D'Aoust,M.A.
        Promoter for regulating expression of foreign genes
        Patent: WO 0125455-A 3 12 APR 2001,
        Medicago Inc. (CA)
        Location/Qualifiers
            1..731
                /organism="synthetic construct"
                /db_xref="taxon:52630"
                /note="Sequence to be used as a Promoter for regulating
expression"
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(ORIGIN

Query Match	54.18;	Score 731;	DB 6;	length 731;
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[illegible]

misc_feature 857..870
/note="box 1: homology"
TATA_signal 903..910
mRNA 940..998
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/product="plastocyanin"
gene 940..998
/gene="petE"
CDS 993..998
/gene="petE"
/codon_start=1
/product="plastocyanin"
/protein_id="CAA48393.1"
/db_xref="GI:4379383"
/translation="MA"
BASIC COUNT 339 a 201 c 154 g 304 t
ORIGIN

Query Match 4.2% Score 57; DB 8; Length 998;
Best Local Similarity 100.0%; Pred. No. 7.6e-18;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 767 agataaccacttaagccagcactctgtgagatcatcatatataatcaca 823
|||||
Db 788 ACATACCCACTTTAGCCACGACACTCTGTGACATTAATTAATACCA 844

RESULT 8
PSPIAS 1505 bp DNA linear PIN 27-MAR-1995
DEFINITION pea gene for plastocyanin.
ACCESSION X16082
VERSION X16082.1 GI:20845
KEYWORDS electron carrier; photosynthesis, plastocyanin.
SOURCE pea
ORGANISM Pisum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciales; Pisum.

REFERENCE 1 (bases 1 to 1505)
AUTHORS Last,D.I. and Gray,J.C.
TITILE Plastocyanin is encoded by a single-copy gene in the pea haploid genome

JOURNAL Plant Mol. Biol. 12, 655-666 (1989)
FEATURES
source Location/Qualifiers
1..1505
/organism="Pisum sativum"
/strain="peitham first"
/db_xref="taxon:3888"
/clone="lambda-GPC3"
/issue-type="Shools"
/clone_lib="lambda FMBL3"

repeat_region 1..46
/note="imperfect direct repeat 1"
repeat_region 21..50
/note="imperfect direct repeat 2"
repeat_region 25..62
/note="imperfect direct repeat 3"
old_sequence 39..41
/note="aca was aga in []"
/citation=[1]
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repeat_region 94..139
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/note="imperfect direct repeat 2"
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/note="imperfect direct repeat 3"

promoter 723..730
/note="pot. TATA box"
misc_feature 758..761
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CDS 813..1319
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/db_xref="SMIS-PROT:P16002"
/translation="MATVSTVAIPSESLKTNAAIKVSAKRIPTSTSQSPICVPLASLKDPGVAVIAASAVIASNALAVIALGASIGGLAVPSSLEVASLIVFKRNA
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MVGQIVN"
transl_peptide 813..1019
mat_peptide 1020..1316
/product="maize plastocyanin (AA 1-99)"
BASIC COUNT 460 a 299 c 283 g 463 t
ORIGIN

Query Match 4.2% Score 57; DB 8; Length 1505;
Best Local Similarity 100.0%; Pred. No. 7.4e-18;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 767 agataaccacttaagccagcactctgtgagatcatcatatataatcaca 823
|||||
Db 608 ACATACCCACTTTAGCCACGACACTCTGTGACATTAATTAATACCA 844

RESULT 9
AX036607 68 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 13 from Patent FR2791358.
ACCESSION AX036607
VERSION AX036607.1 GI:11226202
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct.
artificial sequence.
REFERENCE 1 (bases 1 to 68)
AUTHORS Hance,I., Theissen,M. and Gruber,V.
JOURNAL Patent: FR 2791358-A 13-29-SEP-2000;
MERISTEM THERAPEUTICS (FR)

FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Directional building block S3-Directional building block oligonucleotide for the construction of promoters by 1b-PCR"

BASE COUNT 22 a 19 c 5 g 22 t
ORIGIN

Query Match 2.5% Score 34; DB 5; Length 68;
Best Local Similarity 100.0%; Pred. No. 5.9e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 790 cactctgtgacatcatatataatcaca 823
|||||
Db 12 CACTCTGTGACACATTAATTAATACCA 45

RESULT 10
AX036600 250 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 6 from Patent FR2791358.
ACCESSION AX036600
VERSION AX036600.1 GI:11226195
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct.

REFERENCE 1 (bases 1 to 303)
 AUTHORS Rance, I., Theisen M. and Gruber, V.
 JOURNAL Patent: FR 2791358-A 8 29-SEP-2000;
 MERISTEM THERAPEUTICS (FR)

FEATURES
 source
 1..303
 Location/Qualifiers

promoter
 1..303
 /db_xref="taxon:32630"
 /note="The promoter Mp1153 was obtained by fusing a
 sequence of 78 bp of the promoter pelE, stretching from
 position -582 to position -510 bp modified by ad. junction
 of a 'G' box
 Promoter Mp1153"

BASE COUNT 101 a 78 c 41 g 83 t
 ORIGIN

Query Match 2.3%; Score 31; DB 6; Length 303;
 Best Local Similarity 100.0%; Proc. No. 0.00018;
 Matches 31, Conservative 0, Mismatches 0; Indels 0; Gaps 0;

QY 790 cactctgtgacacatctatctaatc 820
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 DB 91 cactctgtgacacatctatctaatc 121

RESULT 15
 AX036609

LOCUS AX036609 72 bp RNA Linear FAT 16-NOV-2000
 DEFINITION Sequence 15 from Patent FR2791358.
 ACCESSION AX036609
 VERSION AX036609.1 GI:11226204

KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 LOCATION/Qualifiers

REFERENCE 1 (bases 1 to 72)
 AUTHORS Rance, I., Theisen M. and Gruber, V.
 JOURNAL Patent: FR 2791358-A 15 29-SEP-2000;
 MERISTEM THERAPEUTICS (FR)

FEATURES
 source
 1..72
 Location/Qualifiers

/organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="directional building block S5-directional building
 block oligonucleotide for the construction of promoters by
 Id-PCR"

BASE COUNT 22 a 20 c 10 g 20 t
 ORIGIN

Query Match 2.0%; Score 27; DB 6; Length 72;
 Best Local Similarity 100.0%; Proc. No. 0.023;
 Matches 27, Conservative 0, Mismatches 0; Indels 0; Gaps 0;

QY 794 ctgtgacacatctatctaatc 820
 ||||||||||||||||||||||||||||
 DB 1 ctgtgacacatctatctaatc 27

Search completed: September 1, 2002, 03:06:49
 Job time: 12046 sec



Accession	Gene	Species	Length (bp)	GC (%)	GC (3bp)	GC (6bp)	GC (9bp)	GC (12bp)	GC (15bp)	GC (18bp)	GC (21bp)	GC (24bp)	GC (27bp)	GC (30bp)	GC (33bp)	GC (36bp)	GC (39bp)	GC (42bp)	GC (45bp)	GC (48bp)	GC (51bp)	GC (54bp)	GC (57bp)	GC (60bp)	GC (63bp)	GC (66bp)	GC (69bp)	GC (72bp)	GC (75bp)	GC (78bp)	GC (81bp)	GC (84bp)	GC (87bp)	GC (90bp)	GC (93bp)	GC (96bp)	GC (99bp)	GC (102bp)	GC (105bp)	GC (108bp)	GC (111bp)	GC (114bp)	GC (117bp)	GC (120bp)	GC (123bp)	GC (126bp)	GC (129bp)	GC (132bp)	GC (135bp)	GC (138bp)	GC (141bp)	GC (144bp)	GC (147bp)	GC (150bp)	GC (153bp)	GC (156bp)	GC (159bp)	GC (162bp)	GC (165bp)	GC (168bp)	GC (171bp)	GC (174bp)	GC (177bp)	GC (180bp)	GC (183bp)	GC (186bp)	GC (189bp)	GC (192bp)	GC (195bp)	GC (198bp)	GC (201bp)	GC (204bp)	GC (207bp)	GC (210bp)	GC (213bp)	GC (216bp)	GC (219bp)	GC (222bp)	GC (225bp)	GC (228bp)	GC (231bp)	GC (234bp)	GC (237bp)	GC (240bp)	GC (243bp)	GC (246bp)	GC (249bp)	GC (252bp)	GC (255bp)	GC (258bp)	GC (261bp)	GC (264bp)	GC (267bp)	GC (270bp)	GC (273bp)	GC (276bp)	GC (279bp)	GC (282bp)	GC (285bp)	GC (288bp)	GC (291bp)	GC (294bp)	GC (297bp)	GC (300bp)	GC (303bp)	GC (306bp)	GC (309bp)	GC (312bp)	GC (315bp)	GC (318bp)	GC (321bp)	GC (324bp)	GC (327bp)	GC (330bp)	GC (333bp)	GC (336bp)	GC (339bp)	GC (342bp)	GC (345bp)	GC (348bp)	GC (351bp)	GC (354bp)	GC (357bp)	GC (360bp)	GC (363bp)	GC (366bp)	GC (369bp)	GC (372bp)	GC (375bp)	GC (378bp)	GC (381bp)	GC (384bp)	GC (387bp)	GC (390bp)	GC (393bp)	GC (396bp)	GC (399bp)	GC (402bp)	GC (405bp)	GC (408bp)	GC (411bp)	GC (414bp)	GC (417bp)	GC (420bp)	GC (423bp)	GC (426bp)	GC (429bp)	GC (432bp)	GC (435bp)	GC (438bp)	GC (441bp)	GC (444bp)	GC (447bp)	GC (450bp)	GC (453bp)	GC (456bp)	GC (459bp)	GC (462bp)	GC (465bp)	GC (468bp)	GC (471bp)	GC (474bp)	GC (477bp)	GC (480bp)	GC (483bp)	GC (486bp)	GC (489bp)	GC (492bp)	GC (495bp)	GC (498bp)	GC (501bp)	GC (504bp)	GC (507bp)	GC (510bp)	GC (513bp)	GC (516bp)	GC (519bp)	GC (522bp)	GC (525bp)	GC (528bp)	GC (531bp)	GC (534bp)	GC (537bp)	GC (540bp)	GC (543bp)	GC (546bp)	GC (549bp)	GC (552bp)	GC (555bp)	GC (558bp)	GC (561bp)	GC (564bp)	GC (567bp)	GC (570bp)	GC (573bp)	GC (576bp)	GC (579bp)	GC (582bp)	GC (585bp)	GC (588bp)	GC (591bp)	GC (594bp)	GC (597bp)	GC (600bp)	GC (603bp)	GC (606bp)	GC (609bp)	GC (612bp)	GC (615bp)	GC (618bp)	GC (621bp)	GC (624bp)	GC (627bp)	GC (630bp)	GC (633bp)	GC (636bp)	GC (639bp)	GC (642bp)	GC (645bp)	GC (648bp)	GC (651bp)	GC (654bp)	GC (657bp)	GC (660bp)	GC (663bp)	GC (666bp)	GC (669bp)	GC (672bp)	GC (675bp)	GC (678bp)	GC (681bp)	GC (684bp)	GC (687bp)	GC (690bp)	GC (693bp)	GC (696bp)	GC (699bp)	GC (702bp)	GC (705bp)	GC (708bp)	GC (711bp)	GC (714bp)	GC (717bp)	GC (720bp)	GC (723bp)	GC (726bp)	GC (729bp)	GC (732bp)	GC (735bp)	GC (738bp)	GC (741bp)	GC (744bp)	GC (747bp)	GC (750bp)	GC (753bp)	GC (756bp)	GC (759bp)	GC (762bp)	GC (765bp)	GC (768bp)	GC (771bp)	GC (774bp)	GC (777bp)	GC (780bp)	GC (783bp)	GC (786bp)	GC (789bp)	GC (792bp)	GC (795bp)	GC (798bp)	GC (801bp)	GC (804bp)	GC (807bp)	GC (810bp)	GC (813bp)	GC (816bp)	GC (819bp)	GC (822bp)	GC (825bp)	GC (828bp)	GC (831bp)	GC (834bp)	GC (837bp)	GC (840bp)	GC (843bp)	GC (846bp)	GC (849bp)	GC (852bp)	GC (855bp)	GC (858bp)	GC (861bp)	GC (864bp)	GC (867bp)	GC (870bp)	GC (873bp)	GC (876bp)	GC (879bp)	GC (882bp)	GC (885bp)	GC (888bp)	GC (891bp)	GC (894bp)	GC (897bp)	GC (900bp)	GC (903bp)	GC (906bp)	GC (909bp)	GC (912bp)	GC (915bp)	GC (918bp)	GC (921bp)	GC (924bp)	GC (927bp)	GC (930bp)	GC (933bp)	GC (936bp)	GC (939bp)	GC (942bp)	GC (945bp)	GC (948bp)	GC (951bp)	GC (954bp)	GC (957bp)	GC (960bp)	GC (963bp)	GC (966bp)	GC (969bp)	GC (972bp)	GC (975bp)	GC (978bp)	GC (981bp)	GC (984bp)	GC (987bp)	GC (990bp)	GC (993bp)	GC (996bp)	GC (999bp)	GC (1002bp)	GC (1005bp)	GC (1008bp)	GC (1011bp)	GC (1014bp)	GC (1017bp)	GC (1020bp)	GC (1023bp)	GC (1026bp)	GC (1029bp)	GC (1032bp)	GC (1035bp)	GC (1038bp)	GC (1041bp)	GC (1044bp)	GC (1047bp)	GC (1050bp)	GC (1053bp)	GC (1056bp)	GC (1059bp)	GC (1062bp)	GC (1065bp)	GC (1068bp)	GC (1071bp)	GC (1074bp)	GC (1077bp)	GC (1080bp)	GC (1083bp)	GC (1086bp)	GC (1089bp)	GC (1092bp)	GC (1095bp)	GC (1098bp)	GC (1101bp)	GC (1104bp)	GC
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CC useful for regulating the expression of foreign genes in *Transgenic*
CC organisms, particularly plants, e.g., monocotyledons, dicotyledons or
CC gymnosperms, by preparing a transgenic organism using an expression
CC construct comprising the promoter and an open reading frame (ORF) of a
CC gene.
XX
XX
S0 Sequence 971 bp; 390 A; 141 C; 145 G; 255 T; 0 other;

50 Sequence 971 RP; 390 A; 141 C; 145 G; 295 T; 0 other;

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Query Match      71.98; Score 971; DB 22; Length 971;
Best Local Similarity 100.0%; Pred No 0;
Matches 971; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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OY	9	cggagcttgatarrattatattgtgcacatgaactcaaaaacacataaaagtcttaagtgcac	68
Db	1	cggagctglatattatattatgtlgtlccaataaacccaacaaacacataaagcttlaagttacga	60
OY	69	agcgtctacactttctatttgaacaaatatccactactactgttataatcattatga	128
Db	61	agltgtacacttttctatttctgaacaaatattccgtaactactgttataatarrattatga	120
OY	129	aacattaaagttaaagaatalagatgataaagaacaaagaatgaatgatalatttgaacaaatga	188
Db	121	aacattagatgaagaatattgtattgaagaacaaagaatgataattttgtacaaat	180
OY	189	tttgttgcacatttggagaataatttgttctctcttctcttcttcttggtaaaacattag	248
Db	181	tttgttgcacacttggagaataatttgttctctcttctcttcttcttggtaaaacattag	240
OY	249	agatagagaaaagagagagagatataaacactatctgtgtatgagagagaaagtgtga	308
Db	241	agagagaaaagagagagagatataaacactatctgtgtatgagagagaaagtgtga	300
OY	309	caaaagctgtaccacaaatagltgtacacaaatatactcttgaggagatrtggatatagtataat	368
Db	301	caaaagctgtaccacaaatagltgtacacaaatatactcttgaggagatrtggatatagtataat	360
OY	369	aataaggttaattgtctgttaataataagatagaacgacttagagagatgtaccattaga	428
Db	361	aataaggttattatgtctgttaataataagatagaacgacttagagagatgtaccattaga	420
OY	429	gaattttggcaadctatataaaaagaagaataattatttttaaaattaaagttgaat	488
Db	421	gaattttggcaagtcattataaaaagaagaataattatttttttaaaattaaagttgaat	480
OY	489	catttgtatlaaacatlgatattatttlaaigaatttgaataaagaattgaattaaagttgat	548
Db	481	catttgtatlaaacatlgatattatttgaataatgaataaagaattgaattaaagttgat	540
OY	549	tagtaattagatttgygttaatttgaatttggacatttgaatttccctatatattgccc	608
Db	541	tagtaatttagaatttgygttcaatttgaatttggacatttgaatttccctatatattgccc	600
OY	609	ccatagagtcagttaaactcttttattctatctatctatagatccaataagaagaataagttat	668
Db	601	ccatagagtcagttaaactcttttattctatctatctatagatccaataagaagaataagttat	660
OY	669	attaatccctcccaaaaaaataaacqqlatatttlaacaaaaatctaaagccacgtatgaq	728
Db	661	attaatccctcccaaaaaaataaacqqlatatttctataaaaaatctaaagccacgtatgaq	720
OY	729	gatacacatccatccaacacatgcacacaaatccgtatgagatataccgccctttaaagccac	788
Db	721	gataaacatccatccatccatccatccatccatccatccatccatccatccatccatccatccat	780
OY	789	gcaactctgtgacacatctacatctataatcaacacatctctccacacatctgagccaca	848
Db	781	gcaactctgtgacacatctacatctataatcaacacatctctccacacatctgagccaca	840
OY	849	caaaaacacatccacatctataacccatctctataaaaaatcacacatttggatgtctac	908
Db	841	caaaaacacatccacatctataacccatctctataaaaaatcacacatttggatgtctac	900

960
961 gagagagaatq 971

Pb

QY 969 gaagaanaaq 979

QY

Pb 961 gagagagaatq 971

RESULT	3
AAS02128	
ID	AAS02128 standard; DNA; 731 bp.

AC AAS02128

DT 18-JUL-2001 (first entry)
 VV

De Promoter #3 for regulating expression of foreign genes.

Promoter: *transgenic* Plant: *monocotyledon*; *dicotyledon*; *gymnosperm*; *ds*

synthetic: XX
XX

XX

XX

XX

XX

XX
XX
XX

Vojina I D'August M

XX
W.L.

Novel promoter for

PT plants - more specifically in a real specific manner in transgenic

PS Claim 1; page 9; 9pp; English.

The sequence represents the coding sequence of promoter #3 for regulating expression of foreign genes in transgenic organisms. The promoter is useful for regulating the expression of foreign genes in transgenic organisms, particularly plants, e.g., monocotyledons, dicotyledons or gymnosperms, by preparing a transgenic organism using an expression construct comprising the promoter and an open reading frame (ORF) of a gene.

Sequence 731 BP; 299 A; 113 C; 109 G; 210 T; 0 others;

Query Match	54.1%	Score 731;	DB 22;	Length 741;
Best Local Similarity	100.0%	Prod. No. 5.72-311;		
Matches 731;	Conservative	0;	Mismatches	0;
			Totals	0;
			Gaps	0;

[illegible]

or comprising a G box operably or functionally linked upstream of a CAT box, TATA box and transcription initiation site. The chimeric promoters are used in expression vectors for producing transgenic plants, such as dicotyledonous species, e.g. potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea, rape, beetroot, or sunflower, and monocotyledonous species, e.g. wheat, barley, oat, rice, or corn.

Sequence 623 BP; 230 A; 128 C; 82 G; 183 T; 0 other;

Query Match 4.2%; Score 57; DB 21; Length 623;

Best Local Similarity 100.0%; Pred. No. 3,2e-15;

Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 767 agataaccacttaagccacgactctgtgacatcatatcctaaacaca 823
 407 agataaccacttaagccacgactctgtgacatcatatcctaaacaca 463

RESULT 6

AAA6457

ID AAA6457 standard; DNA; 834 BP.

AC AAA6457;

DT 08-FEB-2001 (first entry)

DE Nucleotide sequence of the pete promoter from plastocyanin gene

KW pete promoter; chimeric promoter; transgenic plant;

KM plastocyanin gene promoter; ss.

OS Pisum sativum.

PN W0200056906-A1.

XX 28-SEP-2000.

PF 20-MAR-2000; 2000WO-1B00317.

PR 22-MAR-1999; 99FR-0003635.

XX (MERI-) MERISTEM THERAPEUTICS.

PI Rance I, Gruber V, Theisen M;

WP1; 2000-587667/55.

PT Chimeric expression promoter for producing dicotyledonous and

PT monocotyledonous transgenic plants comprises a nucleic acid sequence

derived from a promoter of the pea plastocyanin gene

Claim 1; Page 65; 83pp; English.

The present sequence represents the pete promoter from the pea plastocyanin gene. The promoter directs cell-specific but not full light-regulated expression in transgenic tobacco plants. The promoter is used to construct chimeric promoters of the invention. The specification describes a chimeric expression promoter comprising a promoter of the pea plastocyanin gene, or comprising a G box operably or functionally linked upstream of a CAT box, TATA box and transcription initiation site. The chimeric promoters are used in expression vectors for producing transgenic plants, such as dicotyledonous species, e.g. potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea, rape, beetroot, or sunflower, and monocotyledonous species, e.g. wheat, barley, oat, rice, or corn.

Sequence 834 BP; 289 A; 175 C; 133 G; 237 T; 0 other;

Query Match 4.2%; Score 57; DB 21; Length 834;

Best Local Similarity 100.0%; Pred. No. 3,1e-15;

Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 767 agataaccacttaagccacgactctgtgacatcatatcctaaacaca 824

618 agataaccacttaagccacgactctgtgacatcatatcctaaacaca 674

RESULT 7

AAA6468

ID AAA6468 standard; DNA; 68 BP.

AC AAA6468;

DT 08-FEB-2001 (first entry)

DE Nucleotide sequence of the directional building block S1.

KW pete promoter; chimeric promoter; transgenic plant; MPT1108;

KM plastocyanin gene promoter; PCR primer; ss.

OS Synthetic.

PN W0200056906-A1.

XX 28-SEP-2000.

PF 20-MAR-2000; 2000WO-1B00317.

PR 22-MAR-1999; 99FR-0003635.

XX (MERI-) MERISTEM THERAPEUTICS

PI Rance I, Gruber V, Theisen M;

WP1; 2000-587667/55.

PT Chimeric expression promoter for producing dicotyledonous and

PT monocotyledonous transgenic plants comprises a nucleic acid sequence

derived from a promoter of the pea plastocyanin gene

Claim 24; Page 73; 83pp; English.

The present sequence represents the directional building block S1, which is used to construct chimeric promoters of the invention in PCR reactions. The specification describes a chimeric expression promoter comprising a pete promoter of the pea plastocyanin gene, or comprising a G box operably or functionally linked upstream of a CAT box, TATA box and transcription initiation site. The chimeric promoters are used in expression vectors for producing transgenic plants, such as dicotyledonous species, e.g. potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea, rape, beetroot, or sunflower, and monocotyledonous species, e.g. wheat, barley, oat, rice, or corn.

Sequence 68 BP; 22 A; 19 C; 5 G; 22 T; 0 other;

Query Match 2.5%; Score 34; DB 21; Length 68;

Best Local Similarity 100.0%; Pred. No. 4,4e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 767 agataaccacttaagccacgactctgtgacatcatatcctaaacaca 823

12 agataaccacttaagccacgactctgtgacatcatatcctaaacaca 45

RESULT 8

AAA6462

ID AAA6462 standard; DNA; 250 BP.

AC AAA6462;

DT 08-FEB-2001 (first entry)

DE Nucleotide sequence of the promoter MPT1109.

DR WPI: 2000-587667/55.
 XX
 PT Chimeric expression promoter for producing dicotyledonous and
 PT monocotyledonous transgenic plants comprises a nucleic acid sequence
 PT derived from a promoter of the pea plastocyanin gene
 XX
 PS Claim 2: Page 70; 83pp; English.
 CC The present sequence represents the chimeric promoter Mpr1110. The
 CC promoter is derived from the petE promoter from pea plastocyanin gene
 CC by fusing the petE as-1 like and nos enhancer like elements to the
 CC promoter Mpr1098 (comprising TATA and CAAT boxes of petE), and then
 CC inserting a G box and fusing a fragment of 35S RNA of CMV. The petE
 CC promoter directs cell-specific but not full light regulated expression in
 CC transgenic tobacco plants. The promoter is used to construct chimeric
 CC promoters of the invention. The specification describes a chimeric
 CC expression promoter comprising a promoter of the pea plastocyanin gene,
 CC or comprising a G box operably or functionally linked upstream of a CAAT
 CC box, TATA box and transcription initiation site. The chimeric promoters
 CC are used in expression vectors for producing transgenic plants, such as
 CC dicotyledonous species, e.g. potato, tobacco, cotton, lettuce, tomato,
 CC melon, cucumber, pea, rape, beetroot, or sunflower, and monocotyledonous
 CC species, e.g. wheat, barley, oat, rice, or corn.
 CC
 SQ Sequence 280 BP; 88 A; 73 C; 42 G; 77 T; 0 other;
 XX
 Query Match 2.3%; Score 31; DB 21; Length 280;
 Best Local Similarity 100.0%; Pred. No. 0.00065;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 790 cactctgtgcacatctacattatctaatc 820
 Db 68 cactctgtgcacatctacattatctaatc 98
 ||||||||||||||||||||||||||||||||
 RESULT 11
 AAA96465
 ID AAA96465 standard; DNA; 296 BP
 XX
 AC AAA96465;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Nucleotide sequence of the promoter Mpr1111.
 XX
 KW petE promoter; chimeric promoter; transgenic plant; Mpr1111;
 XX plastocyanin gene promoter; ss.
 OS Synthetic;
 OS Pisum sativum.
 XX
 PN W0200056906-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 20-MAR-2000; 2000WO-1800317
 XX
 PR 22-MAR-1999; 99FR-0003635
 XX
 PA (MERIT-) MERISTEM THERAPEUTICS.
 XX
 PI Rance I, Gruber V, Theisen M.
 XX
 PS WPI: 2000-587667/55.
 XX
 PT Chimeric expression promoter for producing dicotyledonous and
 PT monocotyledonous transgenic plants comprises a nucleic acid sequence
 PT derived from a promoter of the pea plastocyanin gene
 XX
 PS Claim 2: Page 71; 83pp; English.
 CC The present sequence represents the chimeric promoter Mpr1111. The

CC promoter is derived from the petE promoter from pea plastocyanin gene,
 CC by fusing the petE as-1 like and nos enhancer like elements to the
 CC promoter Mpr1098 (comprising TATA and CAAT boxes of petE), and then
 CC inserting a G box and fusing a fragment comprising a duplication of the
 CC element as2 and as1. The petE promoter directs cell-specific but not
 CC full light-regulated expression in transgenic tobacco plants. The
 CC promoter is used to construct chimeric promoters of the invention. The
 CC specification describes a chimeric expression promoter comprising a
 CC promoter of the pea plastocyanin gene, or comprising a G box operably
 CC or functionally linked upstream of a CAAT box, TATA box and transcription
 CC initiation site. The chimeric promoters are used in expression vectors
 CC for producing transgenic plants, such as dicotyledonous species,
 CC e.g. potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea,
 CC rape, beetroot, or sunflower, and monocotyledonous species, e.g. wheat,
 CC barley, oat, rice, or corn.
 CC
 SQ Sequence 296 BP; 94 A; 74 C; 45 G; 83 T; 0 other;
 XX
 Query Match 2.3%; Score 31; DB 21; Length 296;
 Best Local Similarity 100.0%; Pred. No. 0.0084;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 790 cactctgtgcacatctacattatctaatc 820
 Db 84 cactctgtgcacatctacattatctaatc 114
 ||||||||||||||||||||||||||||||||
 RESULT 12
 AAA96464
 ID AAA96464 standard; DNA; 303 BP;
 XX
 AC AAA96464;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Nucleotide sequence of the promoter Mpr1153
 XX
 KW petE promoter; chimeric promoter; transgenic plant; Mpr1153;
 XX plastocyanin gene promoter; ss.
 OS Synthetic;
 OS Pisum sativum.
 XX
 PN W0200056906-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 20-MAR-2000; 2000WO-1800317.
 XX
 PR 22-MAR-1999; 99FR-0003635.
 XX
 PA (MERIT-) MERISTEM THERAPEUTICS.
 XX
 PI Rance I, Gruber V, Theisen M.
 XX
 PS WPI: 2000-587667/55
 XX
 PT Chimeric expression promoter for producing dicotyledonous and
 PT monocotyledonous transgenic plants comprises a nucleic acid sequence
 PT derived from a promoter of the pea plastocyanin gene
 XX
 PS Claim 2: Page 70; 83pp; English.
 CC The present sequence represents the chimeric promoter Mpr1153. The
 CC promoter is derived from the petE promoter from pea plastocyanin gene.
 CC The petE promoter directs cell-specific but not full light-regulated
 CC expression in transgenic tobacco plants. The promoter is used to
 CC construct chimeric promoters of the invention. The specification
 CC describes a chimeric expression promoter comprising a promoter of the
 CC pea plastocyanin gene, or comprising a G box operably or functionally
 CC linked upstream of a CAAT box, TATA box and transcription initiation
 CC site. The chimeric promoters are used in expression vectors for producing

DE Nucleotide sequence of the promoter Mpr1143.
 XX
 KM pete promoter; chimeric promoter; transgenic plant; Mpr1143;
 XX plastocyanin gene promoter; SS.
 XX
 OS Synthetic.
 OS Pisum sativum.
 XX
 PN WO200056906-A1.
 XX
 PD 28-SEP-2000.
 XX
 PE 20-MAR-2000; 2000WO-1B00117.
 XX
 PR 22-MAR-1999; 99FR-0003635.
 XX
 PA (MER-) MERISTEM THERAPEUTICS.
 XX
 PI Rance I, Gruber V, Theissen M;
 PI
 DR MPI: 2000-587667/55.
 XX
 PT Chimeric expression promoter for producing dicotyledonous and
 PT monocotyledonous transgenic plants comprises a nucleic acid sequence
 PT derived from a promoter of the pea plastocyanin gene
 XX
 PS Claim 2: Page 72; 83pp; English.
 XX
 CC The present sequence represents the chimeric promoter Mpr1143. The
 CC promoter is derived from the pete promoter from pea plastocyanin gene,
 CC by fusing the pete as-1 like and nos enhancer like elements to the
 CC promoter Mpr1098 (comprising TATA and CAAT boxes of pete), and then
 CC inserting a G box and fusing a fragment comprising a duplication of the
 CC element as2 and as1. A 72 bp fragment comprising the elements as-2, as-2
 CC and as-1 was then deleted. The pete promoter directs cell-specific but
 CC not full light-regulated expression in transgenic tobacco plants. The
 CC promoter is used to construct chimeric promoters of the invention. The
 CC specification describes a chimeric expression promoter comprising a
 CC promoter of the pea plastocyanin gene, or comprising a G box operably
 CC or functionally linked upstream of a CAAT box, TATA box and transcription
 CC initiation site. The chimeric promoters are used in expression vectors
 CC for producing transgenic plants, such as dicotyledonous species,
 CC e.g. potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea,
 CC rape, beetroot, or sunflower, and monocotyledonous species, e.g. wheat,
 CC barley, oat, rice, or corn.
 XX
 SQ Sequence 220 BP; 73 A; 60 C; 26 G; 61 T; 0 other;

Query Match 1.9%; Score 25; DB 21; Length 220;
 Best Local Similarity 100.0%; Pred. No. 0.37;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 796 gtggacatcatatcataatc 820
 ||||||||||||||||||||
 DB 14 gtggacatcatatcataatc 38

Search completed: September 1, 2002, 03:16:12
 Job time: 8261 sec

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Medicago Genome Initiative accession: MGI:S:21433
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 Plate: 012 row: A column: 10
 Seq primer: TCACACAGCAACAGCATATGAC.
 Location/Qualifiers

FEATURES

source
 1 455
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone="NH012A101"
 /tissue_lib="Phosphate starved leaf"
 /tissue_type="leaf"
 /dev_stage="trifoliolate"
 /note="Vector: lambda Zap; At the trifoliolate stage, M truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoagland's solution containing only 20uM potassium phosphate. RNA was prepared from above ground tissues."
 BASE COUNT 117 a 106 c 104 g 138 t
 ORIGIN

Query Match 10.8%; Score 146; DB 10; Length 455;
 Best Local Similarity 100.0%; Pred. No. 2e-42;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1190 ttgttggtgctgagtgatgaggttgcttgcttcacaaacatttcagatgc 1249
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 DB 234 ttgcttgctgctgctgctgctgctgctgctgctgctgctgctgctg 292
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1250 aagaaagacattacattcaaaacaaacgctgctgctgctgctgctgctg 1009
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 293 GCAGACACCATTTACATTCAGACAAACCTGCTGCTGCTGCTGCTGCTGCTGCTG 352
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1310 gagagattccagaggggttgatgc 1335
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 353 GACGAGATTGAAAGAGAGATTGATG 378
 ||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 9

LOCUS Bf520824 464 bp mRNA linear EST 08-DEC-2000
 DEFINITION EST458297 DStL Medicago truncatula cDNA clone pDStL-2303, mRNA
 sequence.
 ACCESSION Bf520824
 VERSION Bf520824.1 GI:11609507
 KEYWORDS EST.
 SOURCE barrel medic
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eucosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago
 1 (bases 1 to 464)
 Pedrovina M., Pierson R.L., Samadpour A., Vamerni P., Gantner S., Peng
 H., Ellis L., Town C.D., Bowman C.L., Craven M.B., Hansen T.S.,
 Holt, L.E. and Fraser, C.M.
 ESTs from leaves of Medicago truncatula after inoculation with
 Colletotrichum trifolii
 Unpublished (2000)
 Contact: Deborah A. Samadpour
 Department of Plant Pathology
 University of Minnesota
 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
 Tel: 612 625 1243
 Fax: 651 649 5056
 Email: debbysam@tc.umn.edu
 University of Minnesota name: M278256c
 Tick sequence name: M278256c
 More information is available at: <http://olyst.lct.tamu.edu/medicago>
 Seq primer: SKMD (CTA GAA GTG GAT CC).
 Location/Qualifiers

FEATURES

source
 1 464

/organism="Medicago truncatula"
 /cultivar="genotype A17"
 /db_xref="taxon:3880"
 /clone="pDStL-2303"
 /tissue_lib="DStL"
 /tissue_type="leaves infected with Colletotrichum trifolii"
 /dev_stage="cotyledons and primary leaves harvested 5 and 8 days after inoculation with Colletotrichum trifolii"
 /lab_host="E. coli strain XL10L"
 /note="Vector: pUCscript SK-; Site 1: EcoRI; Site 2: XhoI; cDNA was prepared from polyA+ enriched RNA from cotyledons and primary leaves harvested 5 and 8 days after inoculation with Colletotrichum trifolii. The cDNA was directionally ligated into the Uni ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda ZAP phage using Ex Aestri helper phage and propagated in XL10L cells. Note: EST may be of fungal origin."
 BASE COUNT 121 a 108 c 105 g 130 t
 ORIGIN

Query Match 10.8%; Score 146; DB 10; Length 464;
 Best Local Similarity 100.0%; Pred. No. 1.9e-42;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1300 ttt 1249
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 DB 225 ttt 284
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 OY 1250 gagagacacattacattcaaaacaaacgctgctgctgctgctgctgctg 1109
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 DB 285 GCACACACCATTTACATTCAGACAAACCTGCTGCTGCTGCTGCTGCTGCTGCTG 344
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1310 gagagattccagaggggttgatgc 1335
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 345 GACGAGATTGAAAGAGAGATTGATG 370
 ||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 10

LOCUS RE316929 474 bp mRNA linear EST 21-DEC-2000
 DEFINITION NF053806LFP1645 Developing leaf Medicago truncatula cDNA clone
 sequence.
 ACCESSION RE316929
 VERSION RE316929.2 GI:11962636
 KEYWORDS EST.
 SOURCE barrel medic
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eucosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago
 1 (bases 1 to 474)
 Flores-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Holt, C.J.,
 Flores, H.R., Jaman, J.W., Wollert, J.W. and May, G.D.
 Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 Medicago truncatula leaf library
 Unpublished (2000)
 Contact: May GD
 on Jul 14, 2000 this sequence version replaced at: 0196706.

COMMENT

Contact: May GD
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7391
 Fax: 580 221 7380
 Email: gmay@noble.org
 Medicago Genome Initiative accession: MGI:S:21826
 Insert Length: 663 Std Error: 0.00
 Plate: 053 row: B column: 06
 Seq primer: TCACACAGCAACAGCATATGAC.

QY 1250 ggaagaccattacattccagaacatgctggttctccagaacagtatattctgagtaa 1309
 |||||||
 Db 124 GGAACACACATTCATATCCAGACAAGAGTGGTTTCTCCACCACTTATCTTCGATCAA 183
 |||||||

QY 1310 gacagatccaaagcgggttgatgc 1335
 |||||||

Db 184 GAGGAGATTCGAAAGGAGGCTTGATGC 209
 |||||||

RESULT 13

BE633611
 LOCUS BE633611 482 bp mRNA linear EST 19-DEC-2000
 DEFINITION NF058C04DT1F1034 Drought Medicago truncatula cDNA clone NF058C04DT
 5', mRNA sequence.
 ACCSSION BE633611
 VERSION BE633611.1 GI:11897769
 KEYWORDS EST.
 ORGANISM Medicago truncatula
 barrel medic.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.
 1 (bases 1 to 482)
 Authors: Torres-Jerez, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.D.,
 Flores, H.R., Iman, J.T., Weller, J.W. and May, G.D.
 Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 Medicago truncatula drought library
 Unpublished (2000)
 CONTACT: May GD
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7391
 Fax: 580 221 7380
 Email: gdmay@noble.org
 Insert Length: 482 Std Error: 0.00
 Plates: 058 row: C column: 04
 Seq primer: TCACACACCAAAACCTATACAC
 Location/Qualifiers
 1..482
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone="NF058C04DT"
 /tissue="leaf"
 /tissue_type="Plantlets"
 /dev_stage="Pooled timepoints"
 /note="Vector: Lambda Zap; Contains a mixture of entire
 plantlets harvested in a series of days post-watering
 timepoints."

BASE COUNT 122 a 99 c 110 g 151 t

ORIGIN

Query Match 10.8% Score 146; Dh 10; Length 482;
 Best local Similarity 100.0%; Pred. No. 1,9e-42;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 ttgcttgatgctagaaatgagatgagatgcttcttctcagaacatttcacatgagatgc 1249
 |||||||
 Db 149 TTGCTTGAGGCTTAGATGATGAGGATTTGATTTTAAATATTTTAAATGAAATGAG 208
 |||||||

QY 1250 ggaagaccattacattccagaacatgctggttctccagaacagtatattctgagtaa 1309
 |||||||
 Db 209 GGAACACACATTCATATCCAGACAAGAGTGGTTTCTCCACCACTTATCTTCGATCAA 255
 |||||||

QY 1310 gacagatccaaagcgggttgatgc 1335
 |||||||

Db 269 GAGGAGATTCGAAAGGAGGCTTGATGC 294
 |||||||

RESULT 14

BE316878
 LOCUS BE316878 512 bp mRNA linear EST 21-DEC-2000
 DEFINITION NF067H081F1064 Developing leaf Medicago truncatula cDNA clone
 NF067H081F 5', mRNA sequence.
 ACCSSION BE316878
 VERSION BE316878.2 GI:11960234
 KEYWORDS EST.
 ORGANISM Medicago truncatula
 barrel medic.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.
 1 (bases 1 to 512)
 Authors: Torres-Jerez, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.D.,
 Flores, H.R., Iman, J.T., Weller, J.W. and May, G.D.
 Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 Medicago truncatula leaf library
 Unpublished (2000)
 CONTACT: May GD
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7391
 Fax: 580 221 7380
 Email: gdmay@noble.org
 Insert Length: 694 Std Error: 0.00
 Plates: 067 row: B column: 08
 Seq primer: TCACTAGGAAACATGATATGAC
 Location/Qualifiers
 1..512
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone="NF067H081F"
 /tissue="leaf"
 /tissue_type="Developing leaf"
 /dev_stage="Pooled developmental"
 /note="Vector: Lambda Zap; Contains a mixture of very
 young, developing, mature and senescing leaves."

BASE COUNT 137 a 119 c 111 g 145 t

ORIGIN

Query Match 10.8% Score 146; Dh 10; Length 512;
 Best local Similarity 100.0%; Pred. No. 1,9e-42;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1160 ttgcttgatgctagaaatgagatgagatgcttcttctcagaacatttcacatgagatgc 1249
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 Db 243 TTGCTTGAGGCTTAGATGATGAGGATTTGATTTTAAATATTTTAAATGAAATGAG 302
 |||||||

QY 1250 ggaagaccattacattccagaacatgctggttctccagaacagtatattctgagtaa 1309
 |||||||
 Db 303 GGAACACACATTCATATCCAGACAAGAGTGGTTTCTCCACCACTTATCTTCGATCAA 402
 |||||||

QY 1310 gacagatccaaagcgggttgatgc 1335
 |||||||

Db 363 GAGGAGATTCGAAAGGAGGCTTGATGC 388
 |||||||

RESULT 15

BE632144
 LOCUS BE632144 516 bp mRNA linear EST 19-DEC-2000
 DEFINITION NF033F10C21F1080 Drought Medicago truncatula cDNA clone NF033F10C21
 5', mRNA sequence.
 ACCSSION BE632144
 VERSION BE632144.1 GI:11946302
 KEYWORDS EST.
 ORGANISM Medicago truncatula
 barrel medic.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
Rosidae: eurosids 1: Dipsacales: Fattoriaceae: Papilionoideae: Fabulaceae:
Medicago.

REFERENCE
1. (bases 1 to 52)

AUTHORS
Torres Jerez, L., Soto, A.D., Rottis, A.K., Gonzales, R.A., Bell, C.L.,
Flores, H.R., Jimenez, L., Meloy, J.W. and May, G.D.

TITLE
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula de novo library

JOURNAL
Unpublished (2000)

COMMENT
Contact: May 00

Plant Biology Division
The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Phone: 580 221 7091

Fax: 580 221 7080

Email: gdmay@noble.org

Insert length: 516

Plate: 043 row: 1 column: 10

Seq primer: TCACAACCAACACATACAG

FEATURES

Source

1..516

Location: "Medicago truncatula"

Gene: "Medicago"

Feature: "Plant"

Abv: "Stem"

Node: "Vector"

Plant: "Medicago"

Insert: "516"

Plate: "043"

Row: "1"

Column: "10"

Seq primer: "TCACAACCAACACATACAG"

Source: "Medicago truncatula"

Gene: "Medicago"

Feature: "Plant"

Abv: "Stem"

Node: "Vector"

Plant: "Medicago"

Insert: "516"

Plate: "043"

Row: "1"

Column: "10"

Seq primer: "TCACAACCAACACATACAG"

Source: "Medicago truncatula"

Gene: "Medicago"

Feature: "Plant"

Abv: "Stem"

Node: "Vector"

Search completed: September 3, 2002, 01:57:40

Job time: 10:56:50

Query Match

Host Local Similarity

Matches: 146

Conservative

Score: 146

LR: 146

Length: 516

Indels: 0

Gaps: 0

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0%

0%

0%

0%

0%

0%

0%

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0%

RESULT 5
US-08-820-980-1
Sequence 1, Application US/08820980
Patent No. 5923388
GENERAL INFORMATION:
APPLICANT: Sylvain Moineau, Shirley A.
APPLICANT: Walker, Ebenezer R. Vedamuthu,
APPLICANT: and Peter A. Vandenberg
TITLE OF INVENTION: Isolated DNA Encoding
Enzyme For Phage
TITLE OF INVENTION: Resistance
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian G. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
STATE: Michigan
COUNTRY: USA
ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 KB
MEDIUM TYPE: Storage
COMPUTER: Acer
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,980
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,641
FILING DATE: April 19, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ian G. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: Quest 4.1-156
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
TELEX: No. 5925388e
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2987 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE:
US-08-820-980-1

Query Match 1.4% Score 19; DB 2; Length 2987;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 515 atgaattgataaagatt 533
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Db 1446 ATGAATTGATGAAGAGTT 1464

RESULT 6
US-08-826-439-1
Sequence 1, Application US/08826439
Patent No. 5972673
GENERAL INFORMATION:
APPLICANT: Sylvain Moineau, Shirley A.
APPLICANT: Walker, Ebenezer R. Vedamuthu,
APPLICANT: and Peter A. Vandenberg
TITLE OF INVENTION: Isolated DNA Encoding
Enzyme For Phage
TITLE OF INVENTION: Resistance
NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian G. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
STATE: Michigan
COUNTRY: USA
ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 KB
MEDIUM TYPE: Storage
COMPUTER: Acer
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/826,439
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,641
FILING DATE: April 19, 1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ian G. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: Quest 4.1-156
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
TELEX: No. 5972673e
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2987 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE:
US-08-826-439-1

Query Match 1.4% Score 19; DB 2; Length 2987;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 515 atgaattgataaagatt 533
|||||
Db 1446 ATGAATTGATGAAGAGTT 1464

RESULT 7
US-08-913-159-1
Sequence 1, Application US/08913159
Patent No. 6300109
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Plasmid-derived type II
restriction modification systems from lactococcus lactis
NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patcwin Release #1.0, Version #1.30 (1990)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,159
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/079,995
FILING DATE: 17-FEB-1995
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3695 base pairs
TYPE: nucleic acid
STRANDEDNESS: double


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OTHER INFORMATION: /evidence- EXPERIMENTAL
OTHER INFORMATION: /gene- "ORF"
OTHER INFORMATION: /number- 2
OTHER INFORMATION: /s_standard_name- "Gene coding for M.LlaAIb"
OTHER INFORMATION: /label- m-11aAIb
US-08-913-159-5

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Query Match 1.4%; Score 19; DB 4; Length 3695;

Best Local Similarity 100.0%; Prod. No. 17; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0;

QY 515 atgaatgataaagatt 533
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DB 2118 ATGATGATGAAAGATT 2136

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RESULT 10
US-08-913-159-7
Sequence 7, Application US/08913159
Patent No. 6300109
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Plasmid-derived type II
restriction modification systems from Lactococcus lactis
NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EMO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 15/08/913.159
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 1K 0179/95
FILING DATE: 17-FEB-1995
INFORMATION FOR SEQ ID NO. 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3695 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULAR TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Lactococcus lactis subsp. cremoris
STRAIN: W9
FEATURES:
NAME/KEY: CDS
LOCATION: 2412..3323
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /codon_start= 2412
OTHER INFORMATION: /product= "LlaAI restriction endonuclease"
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ORF"
OTHER INFORMATION: /number= 3
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OTHER INFORMATION: /label= r-11aAI
US-08-913-159-7

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Best Local Similarity 100.0%; Prod. No. 17; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0;

QY 515 atgaatgataaagatt 533
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DB 2118 ATGATGATGAAAGATT 2136

RESULT 11

US-09-128-155-16/C

Sequence 16, Application US/09128155

Patent No. 6117654

GENERAL INFORMATION:

APPLICANT: Pan, Yang

TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

FILE REFERENCE: 09434/062001

CURRENT APPLICATION NUMBER: US/09/128,155

EARLIER FILING DATE: 1998-08-03

EARLIER APPLICATION NUMBER: US 60/091,650

EARLIER FILING DATE: 1998-07-02

EARLIER APPLICATION NUMBER: US 60/054,646

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 16

LENGTH: 152331

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)..(152331)

OTHER INFORMATION: n - A,T,C or G

US-09-128-155-16

Query Match 1.4%; Score 19; DB 3; Length 152331;

Best Local Similarity 100.0%; Prod. No. 14; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0;

QY 1268 aagacaaatgctgatttc 1286
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DB 63516 AAGAACAAATGCTGATTTC 63498

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RESULT 12
US-09-128-155-17
Sequence 17, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/062001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 17
LENGTH: 176373
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(176373)
OTHER INFORMATION: n - A,T,C or G
US-09-128-155-17

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Query Match 1.4%; Score 19; DB 3; Length 176373;

Best Local Similarity 100.0%; Prod. No. 13; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0;

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|||||

DB 108094 aagacaaatgctgatttc 108112

RESULT 14
US 09 477 584 10/00
Sequence 10: Application US/09/477584A
Patent No. 6177611
GENERAL INFORMATION:
APPLICANT: Rivo, Douglas A.
TITLE OF INVENTION: Construct of Matrix Protein
FILE REFERENCE: 9718 33, 04/07/97/4775818
CURRENT APPLICATION NUMBER: 09/09/477584A
CURRENT FILING DATE: 1999 07 25
EARLIER APPLICATION NUMBER: 6,207,085
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent In Ver 1.0
SEQ ID NO 10
LENGTH: 565
TYPE: DNA
ORGANISM: Zoa mays
FEATURE:
OTHER INFORMATION: speed promot
US 09 477 584 10

Query Match 1 48: Score 18: 18 4: Length 565:
Best Local Similarity 10.000 Prod No. 502
Matches 18: Conservation 0: Mismatches 0: Indels 0: Gaps 0:

07 2 gagagagagagagat 19
10 565 GAGAGAGAGAGAGAT 19M

RESULT 14
US 09 477 648 4/00
Sequence 4: Application US/09/477648
Patent No. 6,255,529
GENERAL INFORMATION:
APPLICANT: Lappeard, Kathryn
APPLICANT: Mattino, Cathy Susan
TITLE OF INVENTION: Speed promoted promoters
FILE REFERENCE: 0069
CURRENT APPLICATION NUMBER: 09/09/477648
CURRENT FILING DATE: 1999 08 15
EARLIER APPLICATION NUMBER: US 90/097,233
EARLIER FILING DATE: 1998 08 12
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 921
TYPE: DNA
ORGANISM: Zoa mays
FEATURE:
NAME/KEY: Promoter
LOCATION: (1) - (922)
US 09 477 648 4

Query Match 1 48: Score 18: 18 4: Length 921:
Best Local Similarity 10.000 Prod No. 502
Matches 18: Conservation 0: Mismatches 0: Indels 0: Gaps 0:

07 1 gagagagagagat 18
10 890 GAGAGAGAGAGAT 18M

RESULT 15
US 08 478 588 15
Sequence 15: Application US/08/478588
Patent No. 668148
GENERAL INFORMATION:
APPLICANT: John, Makiyaka I

TITLE OF INVENTION: TRANSFERRING PLANTS
TITLE OF INVENTION: PROTECTING HETERODIGS FOR XUVASE
NUMBER OF SEQUENCE: 29
CORRESPONDENT ADDRESS:
ADDRESS: Nicholas J. Soay, quarters & handy
STREET: First Wisconsin Plaza, 100 South
STREET: Pickney St
STREET: P.O. Box 2114
CITY: Madison
STATE: WI
COUNTRY: USA
ZIP: 53701 2114
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM pc compatible
OPERATING SYSTEM: pc-pcs/ms dos
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/08/478588
FILING DATE:
CLASSIFICATION: B00
ATTORNEY/AGENT: INFORMATION:
NAME: Soay, Nicholas J.
REGISTRATION NUMBER: 27,486
REFERENCE/REF KEY NUMBER: 11 229 9101 2
TELECOMMUNICATOR INFORMATION:
TELEPHONE: (608) 261-2484
TELEFAX: (608) 251 9166
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1064 base pairs
TYPE: nucleic acid
STRANDNESS: double
TOPLOGY: linear
MULTIPLE TYPE: cDNA
US 08 478-588 15

Query Match 1 48: Score 18: 18 1: Length 1064:
Best Local Similarity 100.000 Prod No. 502
Matches 18: Conservation 0: Mismatches 0: Indels 0: Gaps 0:

07 947 taattaatattatgag 964
10 785 TAATTAAATAATTAA 964M

Search completed: September 1, 2002, 04:12:18
Job time: 0207 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd

OM nucleic - nucleic search, using sw model

Run on September 1 2002, 03:06:49 : Search time 412.93 seconds
(without alignments)
4940 436 M11 ion col: updates/sec

Title: US-09-678-303-2
Perfect score: 971
Sequence: 1 cggcgtgataattatcgt atcctcttctgagagaaatg 971

Scoring table:
Gapop 60 0 Gapext 60 0

Searched: 1797656 seqs: 10463268293 residues

Word size: 0

Total number of hits satisfying chosen parameters: 3535312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: Genbank
1: gb_ba*
2: gb_hg*
3: gb_in*
4: gb_ov*
5: gb_ov*
6: gb_pat*
7: gb_ph*
8: gb_pl*
9: gb_pr*
10: gb_rv*
11: gb_sl*
12: gb_sy*
13: gb_un*
14: gb_vl*
15: em_ba*
16: em_hu*
17: em_hu*
18: em_in*
19: em_mu*
20: em_om*
21: em_or*
22: em_ov*
23: em_pat*
24: em_ph*
25: em_pl*
26: em_ro*
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29: em_vl*
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31: em_hg_inv*
32: em_hg_other*
33: em_hg_inv*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match Length DB ID Description

1	971	100.0	971	6	AX105268	AX105268 Sequence
2	971	100.0	1350	6	AX105267	AX105267 Sequence
3	731	75.3	731	6	AX105269	AX105269 Sequence
4	57	5.9	326	6	AX036597	AX036597 Sequence
5	57	5.9	623	6	AX036596	AX036596 Sequence
6	57	5.9	834	6	AX036595	AX036595 Sequence
7	57	5.9	998	6	PSFEP	X08313 P-sequence
8	57	5.9	1505	8	ESFAS	X13942 P-sequence
9	34	3.5	68	6	AX036607	AX036607 Sequence
10	34	3.5	250	6	AX036600	AX036600 Sequence
11	32	3.3	207	6	AX036598	AX036598 Sequence
12	31	3.2	280	6	AX036601	AX036601 Sequence
13	31	3.2	296	6	AX036603	AX036603 Sequence
14	31	3.2	303	6	AX036602	AX036602 Sequence
15	27	2.8	72	6	AX036609	AX036609 Sequence
16	27	2.8	266	6	AE2982	AE2982 Sequence
17	25	2.6	250	6	AX036604	AX036604 Sequence
18	25	2.6	259	6	AX036616	AX036616 Sequence
19	25	2.6	1716	8	ALFPHY	ALFPHY Sequence
20	25	2.6	1716	8	MO18296	MO18296 Sequence
21	24	2.5	1084	3	AM031455	AM031455 Sequence
22	24	2.5	64957	2	AC083979	AC083979 Sequence
23	24	2.5	105638	10	AC073463	AC073463 Sequence
24	24	2.5	165918	9	AC104185	AC104185 Sequence
25	24	2.5	166181	30	AC021208	AC021208 Sequence
26	24	2.5	169914	2	AC104184	AC104184 Sequence
27	24	2.5	218126	2	AL627083	AL627083 Sequence
28	23	2.4	281	6	AX036599	AX036599 Sequence
29	23	2.4	5239	6	AX345174	AX345174 Sequence
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34	23	2.3	1732	8	AB028402	AB028402 Sequence
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36	22	2.3	91588	9	AF590487	AF590487 Sequence
37	22	2.3	11541	2	AF104295	AF104295 Sequence
38	22	2.3	130893	2	AF104711	AF104711 Sequence
39	22	2.3	139423	8	AF087545	AF087545 Sequence
40	22	2.3	14901	2	AF022043	AF022043 Sequence
41	22	2.3	158030	9	AF357992	AF357992 Sequence
42	22	2.3	160404	9	AF159152	AF159152 Sequence
43	22	2.3	161927	2	AF091812	AF091812 Sequence
44	22	2.3	161131	2	AF034412	AF034412 Sequence
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ALIGNMENTS

RESULT 1	AX105268	971 bp	DNA	Library	FAI 30-APR-2001
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DEFINITION	AX105268				
ACCESSION	AX105268.1	GI:13921418			
VERSION	AX105268.1	GI:13921418			
KEYWORDS					
SOURCE					
ORGANISM					
synthetic construct					
synthetic construct					
artificial sequence					
1 (bases 1 to 971)					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
Promoter for regulating expression of foreign genes					
Patent: WO 0125455-A 2 12-APR-2001					
Medicago Inc. (CN)					
FEATURES					
Source					
1..971					
location/Qualifiers					
organism="synthetic construct"					
/db_xref="taxon:92630"					
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FASTA COUNT 330 a 141 c 145 g 295 t

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DB 1	CGGGTGGGTAATTAATGATGCTGGGAAATACGAAAAAACAATAAGCTTAAGTACCA	60		
UY 61	AGTGTGTAAATTTTATTTTAAAGAAATATATATATATATATATATATATATATATAT	120		
DB 61	AGTGTGTAAATTTTATTTTAAAGAAATATATATATATATATATATATATATATATAT	120		
UY 121	AGCTTGAATTAAGTAAATATATGATGATGATGATGATGATGATGATGATGATGATGAT	180		
DB 121	AGCTTGAATTAAGTAAATATATGATGATGATGATGATGATGATGATGATGATGATGAT	180		
UY 181	TTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	240		
DB 181	TTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	240		
UY 241	AGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAG	300		
DB 241	AGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAG	300		
UY 401	CGGAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	460		
DB 401	CGGAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	460		
UY 461	AAATTAAGGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	520		
DB 461	AAATTAAGGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	520		
UY 481	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	580		
DB 481	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	580		
UY 541	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	600		
DB 541	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	600		
UY 601	CGGAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	660		
DB 601	CGGAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	660		
UY 661	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	720		
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UY 721	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	780		
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UY 841	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	900		
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UY 901	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	960		
DB 901	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	960		
UY 961	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1020		
DB 961	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1020		

Query Match	100.0%	Score 971	DB 52	Length 1050
Host Local Stimilarity	100.0% <td>Prod. No. 09</td> <td></td> <td></td>	Prod. No. 09		
Matches 971	Conserved	0	Mismatches 0	Indels 0
GapS				
UY 1	CGGGTGGGTAATTAATGATGCTGGGAAATACGAAAAAACAATAAGCTTAAGTACCA	60		
DB 1	CGGGTGGGTAATTAATGATGCTGGGAAATACGAAAAAACAATAAGCTTAAGTACCA	60		
UY 61	AGTGTGTAAATTTTATTTTAAAGAAATATATATATATATATATATATATATATATAT	120		
DB 61	AGTGTGTAAATTTTATTTTAAAGAAATATATATATATATATATATATATATATATAT	120		
UY 121	AGCTTGAATTAAGTAAATATATGATGATGATGATGATGATGATGATGATGATGATGAT	180		
DB 121	AGCTTGAATTAAGTAAATATATGATGATGATGATGATGATGATGATGATGATGATGAT	180		
UY 181	TTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	240		
DB 181	TTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	240		
UY 241	AGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAG	300		
DB 241	AGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAG	300		
UY 401	CGGAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	460		
DB 401	CGGAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	460		
UY 461	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	520		
DB 461	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	520		
UY 521	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	580		
DB 521	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	580		
UY 581	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	640		
DB 581	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	640		
UY 641	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	700		
DB 641	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	700		
UY 701	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	760		
DB 701	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	760		
UY 761	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	820		
DB 761	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	820		
UY 821	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	880		
DB 821	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	880		
UY 881	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	940		
DB 881	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	940		
UY 941	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1000		
DB 941	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1000		
UY 1001	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1060		
DB 1001	GAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1060		

[illegible]

RESULT	3				
AX105269					
LOCUS			731 bp	DNA	
DEFINITION	AX105269				
ACCSSION	Sequence 3	from Patent WO0125455.			
VERSION	AX105269				
VERSION	AX105269.1	GI:13921419			

SOURCE	ORGANISM
SYNTHETIC CONSTRUCT	SYNTHETIC CONSTRUCT
SYNTHETIC CONSTRUCT	SYNTHETIC CONSTRUCT
ARTIFICIAL SEQUENCE	ARTIFICIAL SEQUENCE
1 (BASES 1 TO 731)	1 (BASES 1 TO 731)
WAZINA, L. P. AND YAKOVLEV, M. A.	WAZINA, L. P. AND YAKOVLEV, M. A.
PROMOTER FOR REGULATING EXPRESSION OF FOREIGN GENES	PROMOTER FOR REGULATING EXPRESSION OF FOREIGN GENES
PATENT: WO 0125455-A3 12 APR 2001	PATENT: WO 0125455-A3 12 APR 2001
MEDICAGO INC (CA)	MEDICAGO INC (CA)

FEATURES	source	Location/Qualifiers
		1..731
		/organism="Synthetic construct"
		/db_xref="taxon:34630"
		/note="Sequence to be used as a promoter for regulating expression"
BASE COUNT	299 a	104 g 210 t
ORIGIN		113 c

```

Query Match      75.3%; Score 731; DB 6; Length 731;
Best Local Similarity 100.0%; Pred No 0;
Matches 731; Conservative 0; Mismatches 0; Gaps 0;

```

QY 241 agaaagaagaaagaaagaaacacqaaqaatlaaaacacaaatqtaatlaqaaacaaacatllgta 300

Db 1 AGAGAGAAAAAGGAGAAAGGAGAGATAAAAACATAATGTGAGCTATGAGAGAGAGAAAAAGTTGTA 60

QY 301 caaaagatctgaacaaataatgctgcataacatcatctgaagaaatctgcacaaagctacaca 360

Db 61 CAAAAGTTGTACCCAAAATAGTTTGTATATAATATATATGTAGTAAATTTATGAAAAATGATATATA 120

QY 361 aataaagqcttaatttgcgttaataataaagaatgaacgaatlaagaqaatctaccatllaga 420

Db 121 AATTAAGCGTTAATTTCCTGTATAATAAATTAAGCATGACGCAATTAGCAAGATCTACCAATTACA 180

QY 421 gaatlltggcaagctcatcataaaaagaagaataaattatcttlaaaatlaaaagctgaagt 480

De 181 GAATTTTGGCAAGCTCATTTAAAAGAGAAAGATTAATTTTAAAAATTTAAAGTTGAT 240

QY 481 catttgatlaacacatgtgatatttaaatgaatctgaatgaagaagcttgatgaatlaaagctgcat 540

Db	241	CATTGATTTAAATCTGTGATTATTATATGAAATTGATGAAACAGTTGGATTAAAGTTGTAT	400
QY	541	taqtaattagaatttggatgcgaatttaattgaacattgaattgaattctctccatattgccc	600
Db	301	TAGTAATATAGCAATTCGTGTGCAAAATTAAATTGACATTTGATCTCTTCCGTAATATTCGC	460
QY	601	cgatagatcgaattgaatcattttatattatcagatgcgaattgataaaagacgatatt	560
Db	361	CGATGATATATGATTATCTATTTTTATTTATTTATGATGATGAAATGAAATGAAATGAT	420
QY	661	attaatccctcccaaaaaaaaatggatcattcttctgaataatctgaagccatagag	720
Db	421	ATTATTCCTCCCAAAAAAAAAAAGCGTAAATTATTAAGTAAATATGTAAGCCATGAGAG	480
QY	721	gataacatcgaatcgaacgaattgaacacattctatagatgaacacacttcaataaac	780
Db	481	CATTAATCATCATTCGACGCAATCATCAACATTCGTATGAGATTAATGCACTTAAAGCCGAC	540
QY	781	gaactcttggacattatcatatttaatacagaatctctccgcacattgagatgcaga	840
Db	541	GACTCTTGGCAATTTTCACTTATCTTAAATGACATTAATTCGACATGAGGATTA	600
QY	841	caaaacccaatgcgaatttttatccgcattctatataaataatgcgaattttgattctac	900
Db	601	CAAAAACCAATCCGACATCTTATACACCCGATCTGTAIAAAAAATGATACCTTGTGAGCTTAC	660
QY	901	actttgattcctctcaaacacattgaaataagaaagataataataatgaattgaattcct	960
Db	661	ATTGTGATTCCTCTCAAAACGATATCAAAACATCAAGACATTAATTATTAATTGATCTG	720
QY	961	gagagagaaatg 971	
Db	721	GAGAGAAAAATG 731	

[illegible]

KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (Pages 1 to 326).
AUTHORS Rance, I., Thomson, M., and Gruber, V.
JOURNAL Patent: FR 2791358-A 3 29-Sep-2000;
MERISTEM THERAPEUTICS (FR)

promoter

by a deletion in 5' of the repeated insert sequences, of the 'as-1 like' and 'enhancer like' elements borne by two

```

PASH_COUNT      111 a      91 c      38 g      86 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Prod.No. 3.7e-16;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy      759 agataacccacttlaagccacacacactctatgacacatctaatctaatcrrara 815
|||||
|||||
|||||
Db      110 aatataacccatttaagccacacacacactctatgacacatctaatctaatcrraca 166
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Query Matrix	γ_{sim}	Score γ_f	ER γ_e	Length
Test Local Similarity	100.0%	Prod. No.	3,480,162	
Matrices	γ_f	Missed	γ_e	Edits
				γ_e
Q1	75.9	94.6	94.6	6.2
Q2	40.7	84.7	84.7	4.6

[illegible][illegible]

db 91 CACTGCTGCGGACATCTTAAATCAATCA 124

RESULT 11

AX046604

LOCUS AX046604 207 bp DNA 110041 PAT 16 NOV 2000

DEFINITION Sequence 4 from Patent FR2791458

ACCESSION AX046604

VERSION AX046604.1 GI:11226194

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

FEATURES

LOCUS

PROMOTER

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 4.0%

Matches 42 Conservative 0 Mismatches 0 Indels 0 Gaps 0

db 784 CACTGCTGCGGACATCTTAAATCAATCA 815

db 16 CACTGCTGCGGACATCTTAAATCAATCA 47

RESULT 12

AX046601

LOCUS AX046601 280 bp DNA 110041 PAT 16 NOV 2000

DEFINITION Sequence 7 from Patent FR2791458

ACCESSION AX046601

VERSION AX046601.1 GI:11226194

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

FEATURES

LOCUS

PROMOTER

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 4.0%

Matches 42 Conservative 0 Mismatches 0 Indels 0 Gaps 0

db 784 CACTGCTGCGGACATCTTAAATCAATCA 815

db 16 CACTGCTGCGGACATCTTAAATCAATCA 47

RESULT 13

AX046601

LOCUS AX046601 280 bp DNA 110041 PAT 16 NOV 2000

DEFINITION Sequence 7 from Patent FR2791458

ACCESSION AX046601

VERSION AX046601.1 GI:11226194

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

FEATURES

LOCUS

PROMOTER

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 4.0%

Matches 42 Conservative 0 Mismatches 0 Indels 0 Gaps 0

db 784 CACTGCTGCGGACATCTTAAATCAATCA 815

db 16 CACTGCTGCGGACATCTTAAATCAATCA 47

RESULT 14

AX046602

LOCUS AX046602 483 bp DNA 110041 PAT 16 NOV 2000

DEFINITION Sequence 8 from Patent FR2791458

ACCESSION AX046602

VERSION AX046602.1 GI:11226197

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

FEATURES

LOCUS

PROMOTER

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 4.2%

Matches 42 Conservative 0 Mismatches 0 Indels 0 Gaps 0

db 784 CACTGCTGCGGACATCTTAAATCAATCA 815

db 84 CACTGCTGCGGACATCTTAAATCAATCA 114

RESULT 15

AX046603

LOCUS AX046603 296 bp DNA 110041 PAT 16 NOV 2000

DEFINITION Sequence 9 from Patent FR2791458

ACCESSION AX046603

VERSION AX046603.1 GI:11226198

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

FEATURES

LOCUS

PROMOTER

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 4.2%

Matches 42 Conservative 0 Mismatches 0 Indels 0 Gaps 0

db 784 CACTGCTGCGGACATCTTAAATCAATCA 815

db 84 CACTGCTGCGGACATCTTAAATCAATCA 114

RESULT 16

AX046604

LOCUS AX046604 296 bp DNA 110041 PAT 16 NOV 2000

DEFINITION Sequence 9 from Patent FR2791458

ACCESSION AX046604

VERSION AX046604.1 GI:11226198

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

FEATURES

LOCUS

PROMOTER

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 4.2%

Matches 42 Conservative 0 Mismatches 0 Indels 0 Gaps 0

db 784 CACTGCTGCGGACATCTTAAATCAATCA 815

db 84 CACTGCTGCGGACATCTTAAATCAATCA 114

RESULT 17

AX046605

LOCUS AX046605 296 bp DNA 110041 PAT 16 NOV 2000

DEFINITION Sequence 9 from Patent FR2791458

ACCESSION AX046605

VERSION AX046605.1 GI:11226199

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

FEATURES

LOCUS

PROMOTER

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 4.2%

Matches 42 Conservative 0 Mismatches 0 Indels 0 Gaps 0

db 784 CACTGCTGCGGACATCTTAAATCAATCA 815

db 84 CACTGCTGCGGACATCTTAAATCAATCA 114

RESULT 18

AX046606

LOCUS AX046606 296 bp DNA 110041 PAT 16 NOV 2000

DEFINITION Sequence 9 from Patent FR2791458

ACCESSION AX046606

VERSION AX046606.1 GI:11226200

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

FEATURES

LOCUS

PROMOTER

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 4.2%

Matches 42 Conservative 0 Mismatches 0 Indels 0 Gaps 0

db 784 CACTGCTGCGGACATCTTAAATCAATCA 815

db 84 CACTGCTGCGGACATCTTAAATCAATCA 114

Db 91 CACTGTGTGACACATCTACATTAATC 121

RESULT 15

AX036609

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

MERISTEM

THERAPEUTICS (FR)

Location/Qualifiers

1..72

/organism="synthetic construct"

/db_xref="taxon:32630"

/note="directional building block oligonucleotide for the construction of promoters by

1b-PCR"

BASH COUNT

ORIGIN

22 a

20 c

10 g

20 t

Query Match

Best Local Similarity

Matches

27; Conservative

0; Mismatches

0; Inserts

0; Gaps

0;

QY

786

ctgtgacacatctacattatc

aaac 812

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Search completed: September 1, 2002, 03:06:55
Job time: 12052 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd

OM nucleic - nucleic search, using sw model

Run on: September 3, 2002, 03:16:12, Search time: 426.54 seconds
(without alignments)
3608,574 Million cell updates/sec

Title: US-09-678-303-2
Perfect score: 971
Sequence: 1 cggggcgttcattatctatg... activated: 11/24/2002 971

Scoring table:
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Gapop 60.0, Gapex 60.0

Searched: 1736436 seqs: 858457221 positions

Word size: 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

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prod No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	971	100.0	971	Promoter #2 for re
2	971	100.0	22	Promoter #1 for re
3	731	75.3	22	Promoter #3 for re
4	57	5.9	22	Nucleotide sequence
5	57	5.9	22	Nucleotide sequence
6	57	5.9	22	Nucleotide sequence
7	34	3.5	21	Nucleotide sequence
8	34	3.5	21	Nucleotide sequence
9	32	3.3	21	Nucleotide sequence

10	31	3.2	280	21	AAA96463	Nucleotide sequence
11	31	3.2	296	21	AAA96465	Nucleotide sequence
12	31	3.2	303	21	AAA96464	Nucleotide sequence
13	27	2.8	772	21	AAA96470	Nucleotide sequence
14	27	2.8	266	18	AAU77099	Human calyculin plas
15	25	2.6	229	21	AAA96466	Nucleotide sequence
16	25	2.6	259	21	AAA96477	Nucleotide sequence
17	23	2.4	281	21	AAA96461	Nucleotide sequence
18	23	2.4	5239	24	AB132372	Human immune syste
19	21	2.2	730	21	AAA96467	Nucleotide sequence
20	21	2.2	1319	21	AA160830	Human polynucleoti
21	21	2.2	1344	22	AA159044	Human polynucleoti
22	21	2.2	3399	20	AAK93543	Nucleic acid sequ
23	21	2.2	5249	24	AB132249	Human immune syste
24	21	2.2	5549	21	AB132662	Troscophila melano
25	21	2.2	5845	24	AB132300	Human immune syste
26	21	2.2	10763	24	AB132300	Human immune syste
27	21	2.2	25967	22	AB132300	Troscophila melano
28	20	2.1	28	21	AAA96476	Human immune syste
29	20	2.1	330	21	AAA96476	Human immune syste
30	20	2.1	472	20	AA232774	Human secreted exp
31	20	2.1	520	22	AA187842	Pepper plant root
32	20	2.1	670	22	AAK55845	Human immune syste
33	20	2.1	1273	22	AA160174	Human polynucleoti
34	20	2.1	1302	22	AA158378	Human polynucleoti
35	20	2.1	1991	21	AAK34680	Arabidopsis thalia
36	20	2.1	1993	21	AAK34680	Arabidopsis thalia
37	20	2.1	12426	22	AAK46482	Tumour suppressor
38	19	2.0	70	21	AAA96588	Nucleotide sequence
39	19	2.0	379	22	AA187509	Human polynucleoti
40	19	2.0	394	22	AAK38837	Human polynucleoti
41	19	2.0	403	22	AA189682	Human polynucleoti
42	19	2.0	442	22	AA181552	Human polynucleoti
43	19	2.0	441	22	AA189182	Human polynucleoti
44	19	2.0	517	22	AAK43499	Human polynucleoti
45	19	2.0	745	21	AAK74352	Human secreted pro

ALIGNMENTS

RESULT 1	AAK02127	standard; DNA; 971 bp.
XX	AAK02127:	
XX	18-JUN-2001	(first entry)
XX	Promoter #2 for regulating expression of foreign genes.	
XX	Promoter, transgenic plant, modulated; dicotyledon; gymnosperm; ds.	
XX	Synthetic.	
XX	WO200125455-A2.	
XX	12-APR-2001.	
XX	02-OCT-2000; 2000WO-CA01144.	
XX	04-OCT-1999; 99US-0157129.	
XX	(MED1-) MEDICAGO INT.	
XX	Verina L., D'Amour M.	
XX	WPI; 2001 256316/27	
XX	Novel promoter for regulating expression of foreign genes in transgenic	
XX	organisms; more specifically in a host specific manner in transgenic	
XX	plants -	

[illegible][illegible]

XX 08-FEB-2001 (first entry)
 DE Nucleotide sequence of the pete promoter from plastocyanin gene.
 DE pete promoter, chimeric promoter, transgenic plant;
 KW plastocyanin gene promoter; ss.
 XX
 OS Pisum sativum.
 XX
 PN WO200056906-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 20-MAR-2000; 2000WO-1B00317.
 XX
 PR 22-MAR-1999; 99FR-0003635.
 XX
 PA (MERI-) MERISTEM THERAPEUTICS.
 XX
 PI Rance I, Gruber V, Theissen M;
 XX
 DR WPI; 2000-587667/55.
 XX
 PT Chimeric expression promoter for producing dicotyledonous and
 PT monocotyledonous transgenic plants comprises a nucleic acid sequence
 PT derived from a promoter of the pea plastocyanin gene
 PS
 PS Claim 1; Page 65; 83pp; English
 XX
 CC The present sequence represents the pete promoter from the pea
 CC plastocyanin gene. The promoter directs cell-specific but not full
 CC light-regulated expression in transgenic tobacco plants. The promoter
 CC is used to construct chimeric promoters of the invention. The
 CC specification describes a chimeric expression promoter comprising a
 CC promoter of the pea plastocyanin gene, or comprising a 6 box operably
 CC or functionally linked upstream of a CAAT box, TATA box and
 CC transcription initiation site. The chimeric promoters are used in
 CC expression vectors for producing transgenic plants, such as
 CC dicotyledonous species, e.g., potato, tobacco, cotton, lettuce, tomato,
 CC melon, cucumber, pea, rape, beetroot, or sunflower, and monocotyledonous
 CC species, e.g., wheat, barley, oat, rice, or corn.
 CC
 SO Sequence 834 BP; 289 A; 175 C; 133 G; 237 T; 0 other;

Query Match 5 9%; Score 57; FR 21; Length 834;
 Best Local Similarity 100.0%; Pred. No. 166-14;
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 759 agataaccacitlaagccacgactctgtaacatctaatatctaatatcaca 815
 Db 618 agataaccacitlaagccacgactctgtaacatctaatatcaca 674

RESULT 7
 AAA6468
 ID AAA96468 standard; DNA: 68 BP.
 XX
 AC AAA96468;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Nucleotide sequence of the directional building block S3.
 XX
 KW pete promoter; chimeric promoter; transgenic plant; MPr1108;
 KW plastocyanin gene promoter; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO200056906-A1.
 XX
 PD 28-SEP-2000.

XX 20-MAR-2000; 2000WO-1B00317.
 XX
 PR 22-MAR-1999; 99FR-0003635.
 XX
 PA (MERI-) MERISTEM THERAPEUTICS.
 XX
 PI Rance I, Gruber V, Theissen M;
 XX
 DR WPI; 2000-587667/55.
 XX
 PT Chimeric expression promoter for producing dicotyledonous and
 PT monocotyledonous transgenic plants comprises a nucleic acid sequence
 PT derived from a promoter of the pea plastocyanin gene
 PS
 PS Claim 24; Page 73; 83pp; English.
 XX
 CC The present sequence represents the directional building block S3,
 CC which is used to construct chimeric promoters of the invention in
 CC PCR reactions. The specification describes a chimeric expression
 CC promoter comprising a pete promoter of the pea plastocyanin gene, or
 CC comprising a 6 box operably or functionally linked upstream of a
 CC CAAT box, TATA box and transcription initiation site. The chimeric
 CC promoters are used in expression vectors for producing transgenic
 CC plants, such as dicotyledonous species, e.g., potato, tobacco, cotton,
 CC lettuce, tomato, melon, cucumber, pea, rape, beetroot, or sunflower,
 CC and monocotyledonous species, e.g., wheat, barley, oat, rice, or corn.
 CC
 SO Sequence 68 BP; 22 A; 19 C; 5 G; 22 T; 0 other;

Query Match 3.5%; Score 34; DR 21; Length 68;
 Best Local Similarity 100.0%; Pred. No. 96-05;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 762 cactctgtaacatctaatatctaatatcaca 815
 Db 12 cactctgtaacatctaatatctaatatcaca 45

RESULT 8
 AAA96462
 ID AAA96462 standard; DNA: 250 BP.
 XX
 AC AAA96462;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Nucleotide sequence of the promoter MPr1109.
 XX
 KW pete promoter; chimeric promoter; transgenic plant; MPr1109;
 KW plastocyanin gene promoter; ss.
 XX
 OS Synthetic.
 OS Pisum sativum.
 XX
 PN WO200056906-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 20-MAR-2000; 2000WO-1B00317.
 XX
 PR 22-MAR-1999; 99FR-0003635.
 XX
 PA (MERI-) MERISTEM THERAPEUTICS.
 XX
 PI Rance I, Gruber V, Theissen M;
 XX
 DR WPI; 2000-587667/55.
 XX
 PT Chimeric expression promoter for producing dicotyledonous and
 PT monocotyledonous transgenic plants comprises a nucleic acid sequence
 PT derived from a promoter of the pea plastocyanin gene

SO Sequence 280 BP; 88 A; 73 C; 42 G; 77 T; 0 other;

Query Match 3.2%; Score 31; DB 21; Length 280;

Best Local Similarity 100.0%; Pred. No. 0.0015;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 782 cactctgtgacacatctatcataaacc 812

Db 68 cactctgtgacacatctatcataaacc 98

RESULT 11

AAA6465

ID AAA96465 standard; DNA; 296 BP.

AC AAA96465;

DT 08-FEB-2001 (first entry)

DE Nucleotide sequence of the promoter MPr1111.

KM pete promoter, chimeric promoter, transgenic plant; MPr1111;

KW plastocyanin gene promoter; ss.

OS Synthetic.

OS Pisum sativum.

PN W0200056906-A1.

PD 28-SEP-2000.

PE 20-MAR-2000; 2000MO-1B00317.

PR 22-MAR-1999; 99PR-0004635

PA (MER1-) MERISTEM THERAPEUTICS.

PI Rance I, Gruber V, Thelsen M;

DR WPI; 2000-587667/55.

PT Chimeric expression promoter for producing dicotyledonous and

PT monocotyledonous transgenic plants comprises a nucleic acid sequence

PT derived from a promoter of the pea plastocyanin gene

Claim 2; Page 71; 83pp; English.

CC The present sequence represents the chimeric promoter MPr1111. The
CC promoter is derived from the pete promoter from pea plastocyanin gene,
CC by fusing the pete as-1 like and nos enhancer like elements to the
CC promoter MPr1098 (comprising TATA and CAAT boxes of pete), and then
CC inserting a G box and fusing a fragment comprising a duplication of the
CC element as2 and as1. The pete promoter directs cell-specific but not
CC full light-regulated expression in transgenic tobacco plants. The
CC promoter is used to construct chimeric promoters of the invention. The
CC specification describes a chimeric expression promoter comprising a
CC promoter of the pea plastocyanin gene, or comprising a G box operably
CC or functionally linked upstream of a CAAT box, TATA box and transcription
CC initiation site. The chimeric promoters are used in expression vectors
CC for producing transgenic plants, such as dicotyledonous species,
CC e.g. potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea,
CC rape, beetroot, or sunflower, and monocotyledonous species, e.g. wheat,
CC barley, oat, rice, or corn

SO Sequence 296 BP; 94 A; 74 C; 45 G; 83 T; 0 other;

Query Match

3.2%; Score 31; DB 21; Length 296;

Best Local Similarity 100.0%; Pred. No. 0.0015;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 782 cactctgtgacacatctatcataaacc 912

Db 84 cactctgtgacacatctatcataaacc 114

RESULT 12

AAA6464

ID AAA96464 standard; DNA; 303 BP.

AC AAA96464;

DT 08-FEB-2001 (first entry)

DE Nucleotide sequence of the promoter MPr1153

KM pete promoter, chimeric promoter, transgenic plant; MPr1153;

KW plastocyanin gene promoter; ss.

OS Synthetic.

OS Pisum sativum.

PN W0200056906-A1.

PD 28-SEP-2000.

PE 20-MAR-2000; 2000MO-1B00317.

PR 22-MAR-1999; 99PR-0004635.

PA (MER1-) MERISTEM THERAPEUTICS

PI Rance I, Gruber V, Thelsen M;

DR WPI; 2000-587667/55.

PT Chimeric expression promoter for producing dicotyledonous and

PT monocotyledonous transgenic plants comprises a nucleic acid sequence

PT derived from a promoter of the pea plastocyanin gene

Claim 2; Page 70; 83pp; English.

CC The present sequence represents the chimeric promoter MPr1153. The
CC promoter is derived from the pete promoter from pea plastocyanin gene,
CC by fusing the pete promoter directs cell-specific but not full light-regulated
CC expression in transgenic tobacco plants. The promoter is used to
CC construct chimeric promoters of the invention. The specification
CC describes a chimeric expression promoter comprising a promoter of the
CC pea plastocyanin gene, or comprising a G box operably or functionally
CC linked upstream of a CAAT box, TATA box and transcription initiation
CC site. The chimeric promoters are used in expression vectors for producing
CC transgenic plants, such as dicotyledonous species, e.g. potato, tobacco,
CC cotton, lettuce, tomato, melon, cucumber, pea, rape, beetroot, or
CC sunflower, and monocotyledonous species, e.g. wheat, barley, oat, rice,
CC or corn.

SO Sequence 303 BP; 101 A; 78 C; 41 G; 83 T; 0 other;

Query Match

3.2%; Score 31; DB 21; Length 303;

Best Local Similarity 100.0%; Pred. No. 0.0015;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 782 cactctgtgacacatctatcataaacc 812

Db 91 cactctgtgacacatctatcataaacc 121

RESULT 13

AAA6470

ID AAA96470 standard; DNA; 72 BP.

AC AAA96470;

DT 08-FEB-2001 (first entry)

PT derived from a promoter of the pea plastocyanin gene
 XX
 PS Claim 2; Page 72; 83pp; English.
 XX

CC The present sequence represents the chimeric promoter Mpr1143. The
 CC promoter is derived from the petE promoter from pea plastocyanin gene,
 CC by fusing the petE as-1 like and nos enhancer like elements to the
 CC promoter Mpr1098 (comprising TATA and CAAT boxes of petE), and then
 CC inserting a G box and fusing a fragment comprising a duplication of the
 CC element as2 and as1. A 72 bp fragment comprising the elements as-2, as-2
 CC and as-1 was then deleted. The petE promoter directs cell-specific but
 CC not full light-regulated expression in transgenic tobacco plants. The
 CC promoter is used to construct chimeric promoters of the invention. The
 CC specification describes a chimeric expression promoter comprising a
 CC promoter of the pea plastocyanin gene, or comprising a G box operably
 CC or functionally linked upstream of a CAAT box, TATA box and transcription
 CC initiation site. The chimeric promoters are used in expression vectors
 CC for producing transgenic plants, such as dicotyledonous species,
 CC e.g. potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea,
 CC rape, beetroot, or sunflower, and monocotyledonous species, e.g. wheat,
 CC barley, oat, rice, or corn.
 XX

SQ Sequence 440 BP; 73 A; 30 C; 46 G; 61 T; 0 other;

Query Match

2.6%; Score 25; LH 21; Length 220;

Best Local Similarity 100.0%; Pred. No. 0.51;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 788 gtggacattacattataatc 812
 ||||||||||||||||||||
 DB 14 gtggacattacattataatc 38

Search completed: September 1, 2002, 03:16:22
 Job time: 8271 sec



REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 341)	Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, P.A., Bell, C.T., Flores, H.P., Iman, J.T., Weller, J.W. and May, G.D.	Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula leaf library	Unpublished (2000)	On Jul 14, 2000 this sequence version replaced gi:9190043.
CONTACT:	May GD			
Plant Biology Division				
The Samuel Roberts Noble Foundation				
2510 Sam Noble Parkway, Ardmore, OK 73402, USA				
Tel: 580 221 7391				
Fax: 580 221 7380				
Email: gdmay@noble.org				
Medicago genome initiative accession: MGI:518233				
Insert Length: 806	Std Error: 0.00			
Plate: 035	row: 6	column: 01		
Seq primer: TCACACACGAGAACACGATATGAC.				
Location/Qualifiers				
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/db_xref="taxon:3880"				
/clone="AF035F0111"				
/clone_lib="Developing leaf"				
/tissue_type="leaf"				
/note="stage="Pooled developmental"				
/dev_stage="Pooled developmental"				
/library="Vector: lambda gap. Contains a mixture of very				
young, developing, mature and senescing leaves"				
BASE COUNT	90 a	81 c	73 g	97 t
ORIGIN				
Query Match				
Best Local Similarity	3.0%	Score 29	DB 10	Length 341
Matches	29	Conservative	0	Mismatches 0
Indels	0	Gaps	0	
OY	918	acacatcacagaagagaagctaat	946	
Db	16	ACACATCACAGAGAGAGACTAAT	44	
RESULT	5			
LOCUS	B1272586	369 bp	mpna	linear
DEFINITION	NEO22H05F11P047 developing flower			Medicago truncatula cDNA clone
ACCESSION	NEO22H05F11P047			5' mRNA sequence.
VERSION	B1272586			
KEYWORDS	B1272586.1	GI:1482041		
SOURCE	EST			
ORGANISM	Medicago truncatula			
REFERENCE	1 (bases 1 to 369)			
AUTHORS	Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, P.A., Bell, C.T., Flores, H.P., Iman, J.T., Weller, J.W. and May, G.D.			
TITLE	Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula flower library			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: May GD			
	Plant Biology Division			
	The Samuel Roberts Noble Foundation			
	2510 Sam Noble Parkway, Ardmore, OK 73402, USA			
	Tel: 580 221 7391			
	Fax: 580 221 7380			
	Email: gdmay@noble.org			
	Insert Length: 369	Std Error: 0.00		
	Plate: 002	row: 11	column: 05	
	Seq primer: TCACACACGAGAACACGATATGAC.			
	Location/Qualifiers			
FEATURES				

SOURCE	1-369	100 a	87 c	78 g	102 b	2 others
/organism="Medicago truncatula"						
/db_xref="taxon:3880"						
/clone="NF022H05FL"						
/clone="ab" "developing flower"						
/tissue="type" "developing flowers"						
/dev_stage="developmentally pooled"						
very young, developing, fully-opened flowers and flowers						
in early transition into pods."						
/note="Vector: Lambda Zap, cDNA was prepared from polyA-						
enriched, pooled samples of equivalent amounts of total						
RNA from very young, developing, fully opened flowers and						
flowers transitioning into pods. The cDNA was						
directionally ligated into the Zap AR vector						
(Stratagene) and packaged using the Gigapack III Gold						
packaging extracts. Phagemids containing cDNA inserts were						
in vitro excised from the phage-pack. The Zap AR vector						
using Exassist helper phage and the EcoRI strain						
Xba-Hind MRF (Stratagene). Excised plasmids were plated						
using SOLR cells."						

Query Match	3.0%	Score 29	DB 10	Length 359
Post local Similarity	100.0%	Prod. No. 5.2		
Matches 29	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY 918	acacatacacaagatgaagactaat	946		
DB 25	ACACATACCAACACACACACATATAT	53		
RESULT 6				
LOCUS	BI270865	378 bp	RNA	Linear EST 19 JUN 2001
DEFINITION	NF002602PL1P1020	Developing flower	Medicago truncatula cDNA clone	
ACCESSION	NF002602PL1.5	RNA sequence		
VERSION	BI270865			
KEYWORDS	BI270865.1	GI:14878866		
SOURCE	EST			
ORGANISM	barley medic			
	Medicago truncatula			
	Eucalyptol, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,			
	Spermatophyta, Malcolophyta, eudicotyledons, core eudicots,			
	Rosidae, eucosids I, Fabales, Fabaceae, Papilionoideae, Trifoliales,			
	Medicago.			
REFERENCE	1 (bases 1 to 378)			
AUTHORS	James R. Eickholt, Scott A. Lee, Mattias A. G. van der Kooij, R. A. Bell, J. L. Flores, H. R. Iman, J. L. Weller, J. W. and May, O. D.			
TITLE	Expressed Sequence Tags from the Samuel Roberts Noble Foundation			
	Medicago truncatula flower library			
COMMENT	Published (2001)			
	Contact: May OD			
	Plant Biology Division			
	The Samuel Roberts Noble Foundation			
	2510 Sam Noble Parkway, Ardmore, OK 73402, USA			
	Tel: 580 221 7381			
	Fax: 580 221 7380			
	Email: gdmay@noble.org			
	Insert length: 378 Std Error: 0.00			
	Plate: 002 Row: G Column: 02			
	Seq primer: TCACACACGAAACAGCATATGAC			
FEATURES	Location/Qualifiers			
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	/db_xref="taxon:4880"			
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	/clone_id="Developing flower"			
	/library="Developing flowers"			
	/db_xref="developmental:flower"			
	very young, developing, fully opened flowers and flowers			
	in early transition into pods."			

Probe "Vector: Lambda Zap2 cDNA was prepared from poly(A⁺) enriched, pooled samples of equivalent amounts of total RNA from young, developing, fully opened flowers and flowers transitioning into pods. The cDNA was directly ligated into the Zap XR vector (Stratagene) and packaged using the GigaPack 111 Gold packaging extract. Phosphorimager cDNA inserts were in vivo excised from the recombinant Zap XR vector using ExScribe buffer, phage and the T7 coat protein. XI-Minor MR (Stratagene) excision phosphors were plated using Sure-LinkTM.

PAGE COUNT 101 a 69 76 4 112 1

ORIGIN

Query Match 4.0%, Score 29, DB 10, Length 478,
Best Local Similarity 10.0%, Prod. No. 4, 2,
Matches 29, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

918 agcagatgagagagagagagagagatgagat 946
|||||
44 ACAAATAAACAACAAACAATAAATAAT 72

RESULT 7
HE249400 483 bp mRNA linear EST 21 DEC 2000
LOCUS
DEFINITION N014F006L1F1098 local EST from Medicago truncatula cDNA clone
ACCESSION HE249400
VERSION N014F006L1F1098.1
KEYWORDS EST
SOURCE
ORGANISM Medicago truncatula
Eukaryote; Vicialeguminosae; Strophophyllae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Trifoliales; Medicago;
1 (bases 1 to 483)
Author: J. J. Flores, H. K. Juma, L. L. Wolf, J. L. W. and May 2001
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula cDNA library
Unpublished (2000)
on Jul 19, 2000 this sequence version replaced GI:2919461.
Contact: May 01
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7402
Fax: 580 221 7404
Email: juma@noble.org
Insert Length: 670 Std Error: 0.00
Plates: 060 row: 3 column: 12
Seq primer: TTAACAAACAAACAAATAGAAC
Location/Contig: 1 603

REFERENCE
AUTHORS
TITLE
J. J. Flores, H. K. Juma, L. L. Wolf, J. L. W. and May 2001
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula cDNA library
Unpublished (2000)
on Jul 19, 2000 this sequence version replaced GI:2919461.
Contact: May 01
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7402
Fax: 580 221 7404
Email: juma@noble.org
Insert Length: 670 Std Error: 0.00
Plates: 060 row: 3 column: 12
Seq primer: TTAACAAACAAACAAATAGAAC
Location/Contig: 1 603

FEATURES
SOURCE
1..483
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="N014F006L1F1098"
/contig="11b-Typing stem"
/tissue-type="stem"
/low_stage="developing"
/note="Vector: Lambda Zap2 cDNA from a mixture of young, developing, mature and transitioning flowers"

PAGE COUNT 144 a 112 76 4 143 1

ORIGIN

Query Match 4.0%, Score 29, DB 10, Length 483,
Best Local Similarity 10.0%, Prod. No. 4, 5,
Matches 29, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

927 agcagatgagagagagagagagatgagat 946
|||||
64 ACAAATAAACAACAAACAATAAATAAT 92

RESULT 8
AM692904 603 bp mRNA linear EST 20 DEC 2000
LOCUS
DEFINITION N0600125L1F1099 local EST from Medicago truncatula cDNA clone
ACCESSION AM692904
VERSION N0600125L1F1099.1
KEYWORDS EST
SOURCE
ORGANISM Medicago truncatula
Eukaryote; Vicialeguminosae; Strophophyllae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Trifoliales; Medicago;
1 (bases 1 to 603)
Author: J. J. Flores, H. K. Juma, L. L. Wolf, J. L. W. and May 2001
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula cDNA library
Unpublished (2000)
on Aug 14, 2000 this sequence version replaced GI:7676440.
Contact: Juma 01
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7402
Fax: 580 221 7404
Email: juma@noble.org
Insert Length: 670 Std Error: 0.00
Plates: 060 row: 3 column: 12
Seq primer: TTAACAAACAAACAAATAGAAC
Location/Contig: 1 603

REFERENCE
AUTHORS
TITLE
J. J. Flores, H. K. Juma, L. L. Wolf, J. L. W. and May 2001
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula cDNA library
Unpublished (2000)
on Aug 14, 2000 this sequence version replaced GI:7676440.
Contact: Juma 01
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7402
Fax: 580 221 7404
Email: juma@noble.org
Insert Length: 670 Std Error: 0.00
Plates: 060 row: 3 column: 12
Seq primer: TTAACAAACAAACAAATAGAAC
Location/Contig: 1 603

FEATURES
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/clone="N0600125L1F1099"
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/tissue-type="stem"
/low_stage="developing"
/note="Vector: Lambda Zap2 cDNA from a mixture of young, developing, mature and transitioning flowers"

REFERENCE
AUTHORS
TITLE
J. J. Flores, H. K. Juma, L. L. Wolf, J. L. W. and May 2001
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula cDNA library
Unpublished (2000)
on Aug 14, 2000 this sequence version replaced GI:7676440.
Contact: Juma 01
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7402
Fax: 580 221 7404
Email: juma@noble.org
Insert Length: 670 Std Error: 0.00
Plates: 060 row: 3 column: 12
Seq primer: TTAACAAACAAACAAATAGAAC
Location/Contig: 1 603

FEATURES
SOURCE
1..603
/organism="Medicago truncatula"
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/clone="N0600125L1F1099"
/contig="11b-Typing stem"
/tissue-type="stem"
/low_stage="developing"
/note="Vector: Lambda Zap2 cDNA from a mixture of young, developing, mature and transitioning flowers"

PAGE COUNT 144 a 112 76 4 143 1

ORIGIN

Query Match 4.0%, Score 29, DB 10, Length 603,
Best Local Similarity 10.0%, Prod. No. 4,
Matches 29, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

Posidae: eucosids I, Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.

REFERENCE 1 (bases 1 to 611)
 AUTHORS Torres-Jerez, J., Scott, A.D., Harris, A.R., Gonzalez, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula leaf library
 JOURNAL Unpublished (2000)
 COMMENT On Jul 13, 2000 this sequence version replaced gi:9119532.
 CONTACT: May GD
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7391
 Fax: 580 221 7380
 Email: gdmay@noble.org
 Medicago Genome Initiative accession: MGI:S:1581
 Insert Length: 657 Std Error: 0.00
 Plate: 020 Row: B Column: 11
 Seq primer: TCCACCAACAAACAGACACTAATTAAT
 location/Qualifiers
 1..611
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 /db_xref="taxon:3880"
 /clone="NF020811F"
 /clone_lib="Developing leaf"
 /tissue_type="leaf"
 /dev_stage="Pooled developmental"
 /note="Vector. Lambda Zap; Contains a mixture of very young, developing, mature and senescing leaves."

BASE COUNT 164 a 138 c 132 g 177 t

ORIGIN

Query Match 3.0%; Score 29; DB 10; Length 611;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

Oy 918 acacatacaagaagaagactaat 946
 |||||||||||||||||||||||||
 Db 34 ACACATACAAAGACAGACACTAAT 62

RESULT 10
 BG457563 637 bp mRNA linear EST 19-MAR-2001
 LOCUS NF105G07P1.1P1054 phosphate starved leaf Medicago truncatula cDNA
 DEFINITION clone NF105G07P1.5', mRNA sequence.
 ACCESSION BG457563
 VERSION BG457563 1 GI:13380804
 KEYWORDS EST.
 ORGANISM Medicago truncatula
 SOURCE barrel medic.
 Medicago truncatula
 Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons;
 Rosidae, eucosids I, Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.
 1 (bases 1 to 637)
 AUTHORS Liu, J., Scott, A.D., Harris, A.R., Gonzalez, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W., May, G.D. and Harrison, M.J.
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula phosphate-starved leaf library
 JOURNAL Unpublished (2000)
 COMMENT Contact: Harrison MJ
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7325
 Fax: 580 221 7380
 Email: mjharrison@noble.org
 Insert Length: 637 Std Error: 0.00
 Plate: 105 Row: G Column: 07
 Seq primer: TCCACCAACAAACAGACACTAATTAAT

FEATURES
 SOURCE Location/Qualifiers
 1..637
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 /db_xref="taxon:3880"
 /clone="NF105G07P1"
 /clone_lib="Phosphate starved leaf"
 /tissue_type="leaf"
 /dev_stage="Trifoliolate"
 /note="Vector. Lambda Zap; At the trifoliolate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoagland's solution containing only 20mM potassium phosphate. RNA was prepared from above ground tissues."

BASE COUNT 178 a 148 c 128 g 182 t

ORIGIN

Query Match 3.0%; Score 29; DB 10; Length 637;
 Best Local Similarity 100.0%; Pred. No. 3.9;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

Oy 918 acacatacaagaagaagactaat 946
 |||||||||||||||||||||||||
 Db 88 ACACATACAAAGACAGACACTAAT 116

RESULT 11
 BE249343 645 bp mRNA linear EST 12-JUL-2000
 LOCUS NF014C09L1F1069 Developing leaf Medicago truncatula cDNA clone
 DEFINITION NF014C09L1F 5', mRNA sequence.
 ACCESSION BE249343
 VERSION BE249343 1 GI:9119403
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons;
 Rosidae, eucosids I, Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.
 1 (bases 1 to 645)
 AUTHORS Torres-Jerez, J., Scott, A.D., Harris, A.R., Gonzalez, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula leaf library
 JOURNAL Unpublished (2000)
 COMMENT Contact: May GD
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7391
 Fax: 580 221 7380
 Email: gdmay@noble.org
 Medicago Genome Initiative accession: MGI:S:14891
 Insert Length: 645 Std Error: 0.00
 Plate: 014 Row: C Column: 09
 Seq primer: TCCACCAACAAACAGACACTAATTAAT
 location/Qualifiers
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 /tissue_type="leaf"
 /dev_stage="Pooled developmental"
 /note="Vector. Lambda Zap; Contains a mixture of very young, developing, mature and senescing leaves."

BASE COUNT 175 a 136 c 134 g 200 t

ORIGIN

Query Match 3.0%; Score 29; DB 10; Length 645;

JOURNAL
COMMENT

Medicago truncatula leaf library
Unpublished (2000)
On Apr. 14, 2003 this sequence version replaced gi.7558361
Contact: May GN

Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7491
Fax: 580 221 7380
Email: gdmay@noble.org

FEATURES

source

1..359

/organism="Medicago truncatula"

/db_xref="taxon:3880"

/clone_lib="NF016101F"

/clone_lib="Developing leaf"

/tissue_type="leaf"

/dev_stage="Pooled developmental"

/note="Vector: Lambda Zap; Contains a mixture of very

young, developing, mature and senescing leaves."

BASE COUNT

98 a 85 c 75 g 101 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 28; DB 9; Length 359;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 919 cacatcaagaagagagactaatat 946

Db 1 CACATCAAGAAGAGAGACTAATAAT 28

REST LT 15

A0841643

LOCUS

1137356b shotgun sub-library of BAC clone 72F02 Medicago truncatula

genomic clone 72-F-02-084, DNA sequence.

ACCESSION

A0841643

VERSION

A0841643.1 GI:5930668

KEYWORDS

GSS.

SOURCE

ORGANISM

barel medic.

Medicago truncatula

Eukaryota; Viridiplantae; Strophophyta; Embryophyta; Tracheophyta,

Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales;

Medicago.

1 (bases 1 to 468)

REFERENCE

Kim, D., Choi, H., Peng, H., Ellis, L., and Cook, D.

T TLE

BAC survey sequencing of Medicago truncatula (1999c)

Unpublished (1995)

CONTACT: Cook DR

The Crop Biotechnology Center

Texas A&M University

Department of Plant Pathology and Microbiology, Km 120 I-10,

Peterson Bldg, College Station, TX 77843-2132, USA

Tel: 409 845 8743

Fax: 409 862 4790

Email: dcook@ppserver.tamu.edu

Other name: HSC-75-84, date: 7/2/99, Submitted to: The Database of

Genome Survey Sequences (GSS) on 09/27/99; More information is

available at 'http://chrystle.tamu.edu/medicago'.

Seq primer: pUC-C

Class: BAC subclone.

Location/Qualifiers

1..468

/organism="Medicago truncatula"

/cultivar="genotype A17"

/db_xref="taxon:3880"

/clone="72-F-02-084"

/clone_lib="shotgun sub-library of BAC clone 72F02"

/note="Vector: pUC18; BAC survey sequences were obtained

from sheared BAC DNA subcloned into the SmaI site of

pUC18. The template DNA for sequencing was obtained by PCR

using universal primers. Sequencing reactions were primed

from the pUC18 primer site (TGAAGAACATATGACATATGACA)

in the pUC18 polylinker."

BASE COUNT

126 a 69 c 80 g 193 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 28; DB 12; Length 468;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 ataatgtatgtatgtatgtatgtatgtat 299

Db 168 ATTAATGTATGTATGTATGTATGTATGTAT 161

Search comp etcd: September 1, 2002, 01:57:53
Job time: 10700 sec

SeqCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 3, 2002 09:12:18 Search time 97.97 seconds
(without alignments) 2487.850 Million cell updates/sec

Title: US-09-678-303-2

Perfect score: 971

Sequence: 1 cggcctggatattatg aatgattgagagaaatg g71

Scoring table: OLIGO NUC

Gapop 60.0, Gapext 60.0

Searched: 38353 seqs, 122816752 residues

Word size: 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000300606

Post-processing: listing first 45 summaries

Database:

Issued_Patents_NA: *

- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq: *
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
- 5: /cgn2_6/ptodata/1/ina/PCUS.COMB.seq: *
- 6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	20	2.1	25	5 PCT-US91-03680-156	Sequence 156, App
2	19	2.0	1720	3 US-08-705-771-2	Sequence 2, Appl
3	19	2.0	2987	1 US-08-423-641B-1	Sequence 1, Appl
4	19	2.0	2987	2 US-08-820-980-1	Sequence 1, Appl
5	19	2.0	2987	2 US-08-826-430-1	Sequence 1, Appl
6	19	2.0	3695	4 US-08-913-154-1	Sequence 1, Appl
7	19	2.0	3695	4 US-08-913-159-3	Sequence 3, Appl
8	19	2.0	3695	4 US-08-913-159-5	Sequence 5, Appl
9	19	2.0	3695	4 US-08-913-159-7	Sequence 7, Appl
10	18	1.9	1064	1 US-08-378-588-15	Sequence 15, Appl
11	18	1.9	1064	2 US-08-811-054-15	Sequence 15, Appl
12	18	1.9	1064	2 PCT-US94-11121-15	Sequence 15, Appl
13	18	1.9	1270	1 US-08-378-588-23	Sequence 23, Appl
14	18	1.9	1270	1 US-08-811-094-23	Sequence 23, Appl
15	18	1.9	1270	5 PCT-US94-11121-23	Sequence 23, Appl
16	18	1.9	1884	1 US-07-704-288C-1	Sequence 1, Appl
17	18	1.9	1884	1 US-08-379-259-1	Sequence 1, Appl
18	18	1.9	3946	4 US-09-316-080-1	Sequence 1, Appl
19	18	1.9	8456	4 US-08-406-030A-23	Sequence 23, Appl
20	17	1.8	25	5 PCT-US91-03680-155	Sequence 155, App
21	17	1.8	25	5 PCT-US91-03680-157	Sequence 157, App
22	17	1.8	25	5 PCT-US91-03680-158	Sequence 158, App
23	17	1.8	352	4 US-08-396-452-2	Sequence 2, Appl
24	17	1.8	352	4 US-09-169-119-2	Sequence 2, Appl
25	17	1.8	564	4 US-08-617-860B-12	Sequence 12, Appl
26	17	1.8	624	4 US-09-385-982-359	Sequence 359, App
27	17	1.8	723	4 US-09-328-111-338	Sequence 338, App

28	17	1.8	1425	2 US-08-883-515-1	Sequence 18, Appl
29	17	1.8	3035	2 US-08-723-624-18	Sequence 5, Appl
30	17	1.8	3630	4 US-08-474-000A-5	Sequence 5, Appl
31	17	1.8	3630	4 US-08-412-157-5	Sequence 19, Appl
32	17	1.8	3824	2 US-08-723-624-19	Sequence 13, Appl
33	17	1.8	5162	2 US-08-916-917-13	Sequence 13, Appl
34	17	1.8	5162	4 US-09-225-170-13	Sequence 5, Appl
35	17	1.8	4474	4 US-09-117-670-5	Sequence 20, Appl
36	17	1.8	6769	1 US-08-480-784-20	Sequence 20, Appl
37	17	1.8	6769	1 US-08-483-553-20	Sequence 20, Appl
38	17	1.8	6769	1 US-08-487-002-20	Sequence 20, Appl
39	17	1.8	6769	1 US-08-483-554B-20	Sequence 20, Appl
40	17	1.8	6769	1 US-08-488-011B-20	Sequence 20, Appl
41	17	1.8	6769	4 US-08-850-727-20	Sequence 20, Appl
42	17	1.8	6769	5 PCT-US95-10202-20	Sequence 20, Appl
43	17	1.8	6769	5 PCT-US95-10203-20	Sequence 20, Appl
44	17	1.8	6769	5 PCT-US95-10220-20	Sequence 20, Appl
45	17	1.8	17327	1 US-07-906-871-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
PCT-US91-03680-156
Sequence 156, Application PCT/US9103680

GENERAL INFORMATION:
APPLICANT: MATTEUCCI, MARK D.
TITLE OF INVENTION: SEQUENCE-SPECIFIC NONHOMOLOGATED
TITLE OF INVENTION: CROSSLINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF
TITLE OF INVENTION: DUPLEX DNA
CORRESPONDENCE ADDRESSES: 158
ADDRESS: MORRISON & FOERSTER
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/03680
FILING DATE: 19910924
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGO, KATE H.
REGISTRATION/DOCKET NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4610-0011.40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SPO ID NO: 156:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: Single
TOPOLOGY: Linear
PCT-US91-03680-156

Query Match 2.1% Score 20; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Gy 233 agagagagagagagagag 258
Tb 3 AGAGGAGGAGAGAGAGAG 22

RESULT 2

US OR 705 771 2

Sequence 2, Application US 08/05/771

Patent No. 6054289

GENERAL INFORMATION:

APPLICANT: Paul Moore, Robert Gentry, Douglas H.

APPLICANT: Dan M and Clint Shain III

TITLE OF INVENTION: Human genes, Sequen-ces and

TITLE OF INVENTION: Expression Products

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARLEA, JEROME, PAUL, 1111 E. LAM,

ADDRESSEE: GEORGE, STEWART & GUSTEIN

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

STATE: NEW JERSEY

COUNTRY: USA

ZITE: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 4 5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US08/705,771

FILING DATE: August 40 1996

CLASSIFICATION: 506

AFTERBURY/AGENT INFORMATION:

NAME: MILLINS, JAY

REGISTRATION NUMBER: 4,0074

REFERENCE/SECRET NUMBER: 425800 (44) (FBI-96)

TELECOMMUNICATION INFORMATION:

TELEPHONE: 973 994 170

TELEFAX: 973 994 1744

INFORMATION FOR SEQ ID NO: 25

SEQUENCE CHARACTERISTICS:

LENGTH: 1720 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

MODIFIERS: linear

MOLECULE TYPE: DNA

US OR 705 771 2

Query Match

Host Local Similarity: 100.0% Score 192 DB 4 Length 1720

Matches 192 Conservative 07 Mismatches 07 Indels 07 Gaps 07

UY 552 TCAATGAAATTTTAAAT 45

146 644 TCAATGAAATTTTAAAT 605

RESULT 3

US OR 424 641B 1

Sequence 1, Application US/684,404B

Patent No. 5824524

GENERAL INFORMATION:

APPLICANT: SYLVAIN MORGAN, Shirley A.

APPLICANT: Walkey, Elizabeth R. Veldman, B.

APPLICANT: and Peter A. Vandenborgh

TITLE OF INVENTION: Isolated DNA Encoding

TITLE OF INVENTION: Enzyme for Phage

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ian C. McLeod

STREET: 2190 Commons Parkway

CITY: Okemos

STATE: Michigan

COUNTRY: USA

ZITE: 48864

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 400 KB

MEDIUM TYPE: Storage

COMPUTER: Acer

OPERATING SYSTEM: MS DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 08/06/424,641B

FILING DATE: April 29, 1995

CLASSIFICATION: 405

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/066,480

FILING DATE: December 40 1994

CLASSIFICATION: 445

AFTERBURY/AGENT INFORMATION:

NAME: Ian C. McLeod

REGISTRATION NUMBER: 20,941

REFERENCE/SECRET NUMBER: M1 4,1 151

TELECOMMUNICATION INFORMATION:

TELEPHONE: (517) 847-4100

TELEFAX: (517) 847-4104

INFORMATION FOR SEQ ID NO: 12

SEQUENCE CHARACTERISTICS:

LENGTH: 2987 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Double

MODIFIERS: linear

MOLECULE TYPE: Peptide

US OR 424 641B 1

Query Match

Host Local Similarity: 100.0% Score 192 DB 12 Length 2987

Matches 192 Conservative 07 Mismatches 07 Indels 07 Gaps 07

UY 507 ATGATTTGATGAAATTT 525

146 1446 ATGATTTGAAATTT 1404

RESULT 4

US OR 620 980 1

Sequence 1, Application US/080,008B

Patent No. 5925888

GENERAL INFORMATION:

APPLICANT: SYLVAIN MORGAN, Shirley A.

APPLICANT: Walkey, Elizabeth R. Veldman, B.

APPLICANT: and Peter A. Vandenborgh

TITLE OF INVENTION: Isolated DNA Encoding

TITLE OF INVENTION: Enzyme for Phage

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ian C. McLeod

STREET: 2190 Commons Parkway

CITY: Okemos

STATE: Michigan

COUNTRY: USA

ZITE: 48864

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 400 KB

MEDIUM TYPE: Storage

COMPUTER: Acer

OPERATING SYSTEM: MS DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 08/030,980

FILING DATE:

CLASSIFICATION: 405

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/424,641

FILING DATE: April 19, 1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Ian C. McLeod
 REGISTRATION NUMBER: 20,931
 REFERENCE/DOCKET NUMBER: Quest 4.1-156
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (517) 347-4100
 TELEFAX: (517) 347-4103
 TELETYPE: NO 5925388C
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2987 base pairs
 TYPE: Nucleic Acid
 STRANDEDNESS: Double
 TOPOLOGY: Linear
 MOLECULE TYPE:
 US-08-820-980-1

Query Match 2.0% Score 19, EB 2, Length 2987;
 Best Local Similarity 10.0%; Prod. No. 21;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 atgaattgataaagaatt 525
 ||||||||||||||||
 DB 1446 ATGAATTGATGAAGAGTT 1464

RESULT 5
 US-08-826-439-1
 Sequence 1, Application US/08826439
 Patent No. 5972673
 GENERAL INFORMATION:
 APPLICANT: Sylvain Moineau, Shirley A.
 APPLICANT: Walker, Ebenezer R. Vedamuthu,
 APPLICANT: and Peter A. Vandenberg
 TITLE OF INVENTION: Isolated DNA Encoding
 TITLE OF INVENTION: Enzyme For Plaque
 NUMBER OF INVENTIONS: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ian C. McLeod
 STREET: 2190 Commons Parkway
 CITY: Okemos
 STATE: Michigan
 COUNTRY: USA
 ZIP: 48864
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5.25 Inch, 360 Kb
 MEDIUM TYPE: Storage
 COMPUTER: Acer
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER US/08,826,439
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/424,641
 FILING DATE: April 19, 1995
 CLASSIFICATION: 540
 ATTORNEY/AGENT INFORMATION:
 NAME: Ian C. McLeod
 REGISTRATION NUMBER: 20,931
 REFERENCE/DOCKET NUMBER: Quest 4.1-155
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (517) 347-4100
 TELEFAX: (517) 347-4103
 TELETYPE: NO 5972673C
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2987 base pairs

TYPE: Nucleic Acid
 STRANDEDNESS: Double
 TOPOLOGY: Linear
 MOLECULE TYPE:
 US-08-826-439-1

Query Match 2.0% Score 19, EB 2, Length 2987;
 Best Local Similarity 100.0%; Prod. No. 21;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 atgaattgataaagaatt 525
 ||||||||||||||||
 DB 1446 ATGAATTGATGAAGAGTT 1464

RESULT 6
 US-08-913-159-1
 Sequence 1, Application US/08913159
 Patent No. 6300109
 GENERAL INFORMATION:
 APPLICANT:
 TITLE OF INVENTION: Plasmid-derived type II
 TITLE OF INVENTION: restriction modification systems from lactococcus lactis
 NUMBER OF INVENTIONS: 14
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS-DOS/MS-DOOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EP)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/913,159
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PK 0179/95
 FILING DATE: 17-FEB-1995
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3695 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: lactococcus lactis subsp. cremoris
 STRAIN: W9
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 759..1620
 IDENTIFICATION METHOD: experimental
 OTHER INFORMATION: /codon_start= 759
 OTHER INFORMATION: /product= "Llacti-CAATC- N-6-adenine methylase A"
 OTHER INFORMATION: /evidence= EXPERIMENTAL
 OTHER INFORMATION: /gene= "orf"
 OTHER INFORMATION: /number= 1
 OTHER INFORMATION: /standard_name= "Gene coding for M.LlactiA"
 OTHER INFORMATION: /label= m-1lactiA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1613..2419
 IDENTIFICATION METHOD: experimental
 OTHER INFORMATION: /codon_start= 1613
 OTHER INFORMATION: /product= "Llacti-CAATC- adenine methylase B"
 OTHER INFORMATION: /evidence= EXPERIMENTAL
 OTHER INFORMATION: /gene= "orf"
 OTHER INFORMATION: /number= 2
 OTHER INFORMATION: /standard_name= "Gene coding for M.LlactiB"
 OTHER INFORMATION: /label= m-1lactiB
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 2412..3323

[illegible][illegible]

FERMATINI SYSTEM: 10' to S/N

FERMATINI SYSTEM: 10' to S/N

APPLICATION NUMBER: US/08/513,159
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0179/95
FILING DATE: 17-FEB-1995
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3695 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Lactococcus lactis subsp. cremoris
STRAIN: W9
FEATURES:
NAME/KEY: CDS
LOCATION: 2412..3323
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /codon_start= 2412
OTHER INFORMATION: /product= "LlaAI restriction endonuclease"
OTHER INFORMATION: /evidence= "EXPERIMENTAL"
OTHER INFORMATION: /gene= "CkR"
OTHER INFORMATION: /number= 3
OTHER INFORMATION: /standard_name= "Gene coding for LlaAI restriction endonuclease"
OTHER INFORMATION: /label= r-llaAI
US-(8-913-159-7

Query Match
Best Local Similarity 100.0%; DB 4; Length 3695;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 atgaattgataagaggt 525
|||||
DB 218 ATGATTGATGAAAGGT 2136

RESULT 10
US-(8-378-588-15
Sequence 15, Application US/08378588
Patent No. 5608148
GENERAL INFORMATION:
APPLICANT: John, Maliyakal E.
TITLE OF INVENTION: TRANSGENIC COTTON PLANTS
TITLE OF INVENTION: PRODUCING HETEROLOGOUS PHOSPHOLIPASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nicholas J. Seay, Quatles & Brady
STREET: First Wisconsin Plaza, One South
STREET: Pinckney St.,
CITY: Madison
STATE: WI
COUNTRY: USA
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,588
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 11-229-9101-2
TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 251-2484
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1064 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-378-588-15

Query Match
Best Local Similarity 1.9%; Score 18; DB 2; Length 1064;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 939 taattaataataatca 956
|||||
DB 785 TAATTAATTAATTAATCA 802

RESULT 11
US-08-811-094-15
Sequence 15, Application US/08811094
Patent No. 5869720
GENERAL INFORMATION:
APPLICANT: John, Maliyakal E.
TITLE OF INVENTION: TRANSGENIC COTTON PLANTS
TITLE OF INVENTION: PRODUCING HETEROLOGOUS PHOSPHOLIPASE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nicholas J. Seay, Quatles & Brady
STREET: First Wisconsin Plaza, One South
STREET: Pinckney St.,
CITY: Madison
STATE: WI
COUNTRY: USA
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,094
FILING DATE: 03-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/378,588
FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 11-229-9101-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-2484
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1064 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-811-094-15

Query Match
Best Local Similarity 1.9%; Score 18; DB 2; Length 1064;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 939 taattaataataatca 956

Job time: 8223 sec

? INFORMATION FOR SEQ ID NO. 21:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 1270 base pairs
 ? TYPE: nucleic acid
 ? STRANDEDNESS: double
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: DNA (genomic)
 ? US-08-811-094-23

Query Match 1.98; Score 18; DB 5; Length 1270;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 939 taataataataatca 956
 ||||||||||||||||
 Db 991 TAAATAATAATAATCA 1008

RESULT 15
 PCT-US94-11121-23
 ? Sequence 23, Application PC/TUS9411121
 ? GENERAL INFORMATION:
 ? APPLICANT: John, Maliyakal E.
 ? TITLE OF INVENTION: TRANSGENIC COTTON PLANTS
 ? TITLE OF INVENTION: PEI, DRUGS; HEPATOPROTECTORS; PEROXIDASE
 ? NUMBER OF SEQUENCES: 23
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Nicholas J. Scay, Charles & Hardy
 ? STREET: First Wisconsin Plaza, One South
 ? STREET: Pinckney St.,
 ? STREET: P.O. Box 2113
 ? CITY: Madison
 ? STATE: WI
 ? COUNTRY: USA
 ? ZIP: 53701-2113
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent Release #1.0, Version #1.25
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: PCT/US94/11121
 ? FILING DATE:
 ? CLASSIFICATION:
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Scay, Nicholas J.
 ? REGISTRATION NUMBER: 27,386
 ? REFERENCE/DOCKET NUMBER: 11-229-9076-8
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (608) 251-2484
 ? TELEFAX: (608) 251-9166
 ? INFORMATION FOR SEQ ID NO. 23:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 1270 base pairs
 ? TYPE: nucleic acid
 ? STRANDEDNESS: double
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: DNA (genomic)
 ? PCT-US94-11121-23

Query Match 1.98; Score 18; DB 5; Length 1270;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 939 taataataataatca 956
 ||||||||||||||||
 Db 991 TAAATAATAATAATCA 1008

Search completed: September 1, 2002, 03:12:34

VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATP/R/S	source	BANK COUNT	ORIGIN
AX105267.1	GI:13921417			synthetic construct synthetic construct artificial sequence. 1 (bases 1 to 1350)	Velina, L.P. and D'Amusi, M.A.	Promoter for regulating expression of foreign genes	Patent: WO 0125455-A 1 12-APR-2001; Medicago Inc. (CA)	location/Qualifiers 1..1350	/organism="synthetic construct" /db_xref="taxon:32630" /note="Sequence to be used as a promoter for regulating expression"	482 a 236 c 230 g 422 t	

Query Match	100 0%	Score 731	DB 6	length 1350
Best Local Similarity	100 0%	Prod. No.	0	
Matches 731; Conservative	0	Mismatches	0	Caps 0

[illegible]

Db 969 CAGAGAAATG 979

RESULT	4
AX036597	
LOCUS	326 bp DNA
DEFINITION	Sequence 3 from Patent FR2791458.
ACCESSION	AX036597
VERSION	AX036597.1 GI:11226192
KEYWORDS	

ORGANISM	Synthetic construct
REFERENCE	artificial sequence.
AUTHORS	1 (bases 1 to 326)
JOURNAL	Rance), Thiesen, M. and Grubov, V.
	Patent, FR 2791350 A, 3 29-Sep-2000
	MEPSTVTA, thermophilic (vta)

FEATURES	Location/Qualifiers
source	1. . 326

promoter

BASE COUNT
ORIGIN

111 a	91 c	48 g	86 t
-------	------	------	------

Query Match	7.8%	Score 57	DB 6	Length 326
Best Local Similarity	100.0%	Pred. No. 1,20-16		
Matches 57	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	519	agataaccacattaaagcccaagcactctcttqagacatctacattatctcaaaacga	575	
Db	110	AGATTAACCCACATTTAAAGCCCAAGCAATCTGTGGCCCACTCTCAATATATCTAAATCA	166	

RESULT	5
AX036596	
LOCUS	AX036596 623 bp DNA
DEFINITION	Sequence 2 from Patent FR2791358.
ACCESSION	AX036596
VERSION	AX036596.1 GI:11226191
FEATURES	
ORIGIN	
COMMENTS	
REFERENCE	PAT 16-M-V-2000

SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE artificial sequence.
AUTHORS 1 (bases 1 to 623)
JOURNAL Rance, I., Theissen, M. and Gruber, V.
Patent: FR 279156-A 2 29 SEP 2000;
MERISTEM THERAPEUTICS (FR)

```

promoter
    /organism="synthetic construct"
    /db_xref="taxon:12630"
    1..623
    /note="Promoter MP1097 derived from the promoter pore by
    a deletion in 5' of the repeated invert sequences as well
    as the as-1 like box borne on fragment SphI of 212 bp
    promoter MP1097"
    240..128..82..183..t
    240..t
    128..c
    82..g
    183..t

```

Query Match	7.88;	Score 57;	Dh 6;	Length 623;
Post Local Similarity	100.0%;	Prod No 1 To 16;		
Matches 57; Conservative	0;	Mismatches	0;	Gaps 0;
 Y 519 aaataaccacttttaacrtccagcatttctatggtatcatcaaa 576				

repeat_region 21..50
 /note="imperfect direct repeat 2"
 repeat_region 25..62
 /note="imperfect direct repeat 3"
 old_sequence 39..41
 /note="aca was aga in [1]"
 /catalation=[1]
 repeat_region 59..88
 /note="imperfect direct repeat 2"
 repeat_region 94..139
 /note="imperfect direct repeat 1"
 repeat_region 114..142
 /note="imperfect direct repeat 2"
 repeat_region 130..154
 /note="imperfect direct repeat 2"
 repeat_region 134..171
 /note="imperfect direct repeat 3"
 promoter 723..730
 /note="pL. TATA box"
 misc_feature 758..761
 /note="put. transcriptional start site"
 CDS 813..1319
 /note="precursor peptide (AA -69 to 99)"
 /codon_start=1
 /protein_id="CAA34212.1"
 /db_xref="GI:20846"
 /translational="MAVISTIVAIIPSPGLTKNATKVSAMAKIPTSTSPRLCVR
 ASLKDGVALVATASAVIALASNALEVLASDGLAFVPSLEVSAGETVVFNNNA
 GPHNVFDEDEIPAGVDASKISMPEEDLINRGFTYSKLDKGTITRYCSPHOGAG
 MYGOVTYN"

transit_peptide 813..1019
 mat_peptide 1020..1316
 /product="mature plastocyanin (AA 1-99)"
 BASE COUNT 460 a 299 c 283 g 463 t
 ORIGIN

Query Match 7.8%; Score 57; DB 8; Length 1505;
 Best Local Similarity 100.0%; Pred. No. 9; 8c-17;
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 519 agataccacttaagccacactgtgtgacatctaacatctaaatcaca 575
 Db 608 AGATAACCCACTTAAGCCACCTGTGTGACATCTAACATCA 654

RESULT 9
 LOCUS AX036607 68 bp DNA linear PAT 15-NOV-2000
 DEFINITION Sequence 13 from Patent FR2791358.
 ACCESSION AX036607
 VERSION AX036607.1 GI:11226202
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM artificial sequence.
 REFERENCE 1 (bases 1 to 68)
 AUTHORS Rance, I., Theisen, M. and Gruber, V.
 JOURNAL Patent: FR 2791358-A 13-SEP-2000;
 MERISTEM THERAPEUTICS (FR)
 FEATURES
 Location/Qualifiers
 1..68
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Directional building block S3-Directional building
 block oligonucleotide for the construction of promoters by
 1b-PCR"
 BASE COUNT 22 a 19 c 5 g 22 t
 ORIGIN

Query Match 4.7%; Score 34; DB 6; Length 68;

Best Local Similarity 100.0%; Pred No 1 8a-05;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 542 cactctgtgacatctaatatctaaatcaca 575
 Db 12 CACTCTGTGACATCTAATATCTAAATCA 45

RESULT 10
 LOCUS AX036600 250 bp DNA linear PAT 15-NOV-2000
 DEFINITION Sequence 6 from Patent FR2791358.
 ACCESSION AX036600
 VERSION AX036600.1 GI:11226195
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM artificial sequence.
 REFERENCE 1 (bases 1 to 250)
 AUTHORS Rance, I., Theisen, M. and Gruber, V.
 JOURNAL Patent: FR 2791358-A 6-SEP-2000;
 MERISTEM THERAPEUTICS (FR)
 FEATURES
 Location/Qualifiers
 1..250
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 1..250
 /note="The promoter Mpr109 differs from Mpr108 by a
 deletion of 33 bp in the 5' UTR, 11 bp upstream of the
 point -41
 promoter Mpr109"

BASE COUNT 81 a 67 c 31 g 71 t
 ORIGIN

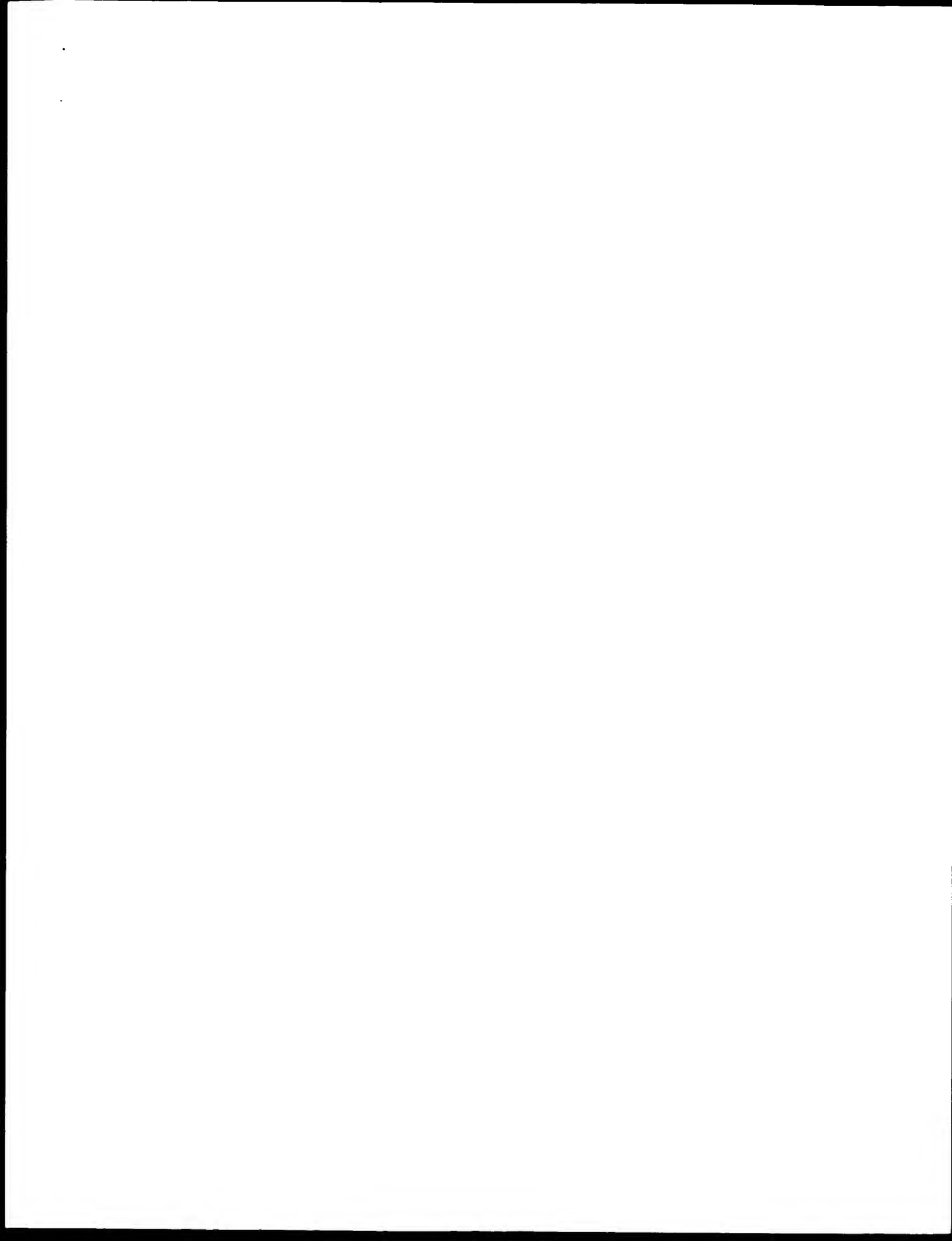
Query Match 4.7%; Score 34; DB 6; Length 250;
 Best Local Similarity 100.0%; Pred No. 1 5a-05;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 542 cactctgtgacatctaatatctaaatcaca 575
 Db 91 CACTCTGTGACATCTAATATCTAAATCA 124

RESULT 11
 LOCUS AX036598 207 bp DNA linear PAT 15-NOV-2000
 DEFINITION Sequence 4 from Patent FR2791358.
 ACCESSION AX036598
 VERSION AX036598.1 GI:11226193
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM artificial sequence.
 REFERENCE 1 (bases 1 to 207)
 AUTHORS Rance, I., Theisen, M. and Gruber, V.
 JOURNAL Patent: FR 2791358-A 4-SEP-2000;
 MERISTEM THERAPEUTICS (FR)
 FEATURES
 Location/Qualifiers
 1..207
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 1..207
 /note="The promoter Mpr109 of 207 bp only contains the
 'TATA' and 'CAAT' boxes and corresponds to a minimal
 reference promoter on the promoter pete.
 promoter Mpr109"
 BASE COUNT 67 a 58 c 21 g 61 t
 ORIGIN

Query Match 4.4%; Score 32; DB 6; Length 207;
 Best Local Similarity 100.0%; Pred. No. 0.00214;

QY 546 ctgtggacatctacattatcttaattc 572
|||||
Db 1 CTGTGGACATCTACATTATCTTAATC 27

Search completed: September 1, 2002, 03:06:59
Job time: 12056 sec



QY	421	attatccctcccaaaaaaaaacggtatatttactaaaaaatctaaagccacgtatgag	480
Db	661	attatccctcccaaaaaaaaacggtatatttactaaaaaatctaaagccacgtatgag	720
QY	481	gataacatccatcccaacacatcacacaacatccctgagatagataacccattaaagccac	540
Db	721	gataacatccatcccaacacatcacacaacatccctgagatagataacccattaaagccac	780
QY	541	gactcgtgagacattatattatattatcaccacattcttcacacattctgagccaca	600
Db	781	gactcgtgagacattatattatattatcaccacattcttcacacattctgagccaca	840
QY	601	caaaaacccatcccatcttattaccccatcttataaaaaatccacatttgaagctacg	660
Db	841	caaaaacccatcccatcttattaccccatcttataaaaaatccacatttgaagctacg	900
QY	661	acttggatcccttcaaacacatacaaaagagaaagacattaaatattaaatcatctt	720
Db	901	acttggatcccttcaaacacatacaaaagagaaagacattaaatattaaatcatctt	960
QY	721	gagagaaaatg	731
Db	961	gagagaaaatg	971
RESULT 3			
ASST	2126		
ID	AAS02126	standard; DNA: 1350 BP.	
XX	ASST2126:		
AC	18-JUN-2001	(first entry)	
XX	Promoter #1 for regulating expression of foreign genes		
DE	Promoter: transgenic plant: monocotyledon, dicotyledon: gymnosperm: ds		
XX	Synthetic.		
OS	WO200125455-A2.		
XX	12-APR-2001.		
XX	02-OCT-2000: 2000WO-CA01144.		
XX	04-OCT-1999: 99US-0157129.		
XX	(MED1-) MEDICAGO INC		
XX	Veizina I., D'Aoust M;		
XX	WPI: 2001-266316/27.		
XX	Novel promoter for regulating expression of foreign genes in transgenic		
XX	organisms, more specifically in a leaf-specific manner in transgenic		
XX	plants -		
XX	Claim 1: Page 8; 9pp; English.		
XX	The sequence represents the coding sequence of promoter #1 for regulating		
XX	expression of foreign genes in transgenic organisms. The promoter is		
XX	useful for regulating the expression of foreign genes in transgenic		
XX	organisms, particularly plants, e.g. monocotyledons, dicotyledons or		
XX	gymnosperms, by preparing a transgenic organism using an expression		
XX	construct comprising the promoter and an open reading frame (ORF) of a		
XX	gene.		
XX	Sequence 1350 BP; 482 A; 236 C; 230 G; 402 T; 0 other;		

Query Match	100.08;	Score 731;	DB 22;	Length 1350
Best Local Similarity	100.08;	Pred. No. 4.9e-297;		

	Matches	731: Conservative	0: Mismatches	0: Indels	0: Gaps					
QY	1	agagagagaaaaaagaagaagagagagatcaaaacacataatgctgctatgagagagagaaatttga	60							
Db	249	agagagagaaaaaagaagaagagagatcaaaacacataatgctgctatgagagagaaatttga	308							
QY	61	caaaagctgacccaagaalagtlgcacaatcattctggaatttgcacaagctacata	120							
Db	309	caaaagctgacccaagaatagttgtatataatctcttgaggaatttgcacaagctacata	368							
QY	121	aataaagtttaattctctgcaaaatcaatgaagagctgaggaattgagagaaatgacattaga	180							
Db	369	aataaagtttaattctctgcaaaatcaatgaagagctgaggaattgagagaaatgacattaga	428							
QY	181	gaatttttgcgaatcattataaaaataaagaataatttttttaatttaaaattgaattgaat	240							
Db	429	gaatttttgcgaatcattataaaaataaagaataatttttttaatttaaaattggaattga	488							
QY	241	catttgaatcaaaagatgattatattaatgaattgaatgaagaatggaattgaattgaat	300							
Db	489	catttgaatcaaaagatgattatattaatgaattgaattgaagaatggaattgaattgaatt	548							
QY	301	tagtaattgaattttggtgcgaatttaattgaattgaatttttttcctatatattgct	360							
Db	549	tagtaattgaattttggtgcgaatttaattgaattgaatttttttcctatatattgct	608							
QY	361	ccatagagctgaatttaactcattttatattctatgaatcaataaagaagaataacgctat	420							
Db	609	ccatagagctgaatttaactcattttatattctatgaatcaataaagaagaataacgctat	668							
QY	421	atttaactctctcaaaaaaaaacacgtatatttataataaaatttaagacctatgaag	480							
Db	669	atttaactctctcaaaaaaaaacacgtatatttataataaaatttaagacctatgaag	728							
QY	481	gataaactccaatccaaccaatccaacaatctcgtatgaataaataacgaattgaagccaat	540							
Db	729	gataaactccaatccaaccaatccaacaatctcgtatgaataaataacgaattgaagccaat	788							
QY	541	gcaactcgtgagcattacattatctaatccacacattctcttcgaacattgaagccaat	600							
Db	789	gcaactcgtgagcattacattatctaatccacacattctcttcgaacattgaagccaat	848							
QY	601	caaaaacccaatccacattcttatccacatttttataaaaaaacacacttttaaaattat	660							
Db	849	caaaaacccaatccacattcttatccacatttttataaaaaaacacacttttaaaattat	908							
QY	661	aatttgattccctccaacaacacataccaagaagaagatataatttaatttaattcattct	720							
Db	909	aatttgattccctccaacaacacataccaagaagaagatataatttaatttaattcattct	968							
QY	721	gagagagaagaatg 731								
Db	969	gagagagaagaatg 979								
RESULT 4										
AAAG6459	Standard: 100A; 326 BP.									
AAAG6459										
08-FEB-2001 (first entry)										
Nucleotide sequence of the promoter MP1096.										
PELE promoter; rhinoidic promoter; transgenic plant, MP1096;										
plastocyanin gene promoter; ss.										
Synthetic.										
Pisum sativum.										
W0200056906-A1.										

CC light-regulated expression in transgenic tobacco plants. The promoter
CC is used to construct chimeric promoters of the invention. The
CC specification describes a chimeric expression promoter comprising a
CC promoter of the pea plastocyanin gene, or comprising a G box operably
CC or functionally linked upstream of a CAAT box, TATA box and
CC transcription initiation site. The chimeric promoters are used in
CC expression vectors for producing transgenic plants, such as
CC dicotyledonous species, e.g. potato, tobacco, cotton, lettuce, tomato,
CC melon, cucumber, pea, rape, beetroot, or sunflower, and monocotyledonous
CC species, e.g. wheat, barley, oat, rice, or corn.

XX Sequence 834 BP: 289 A; 175 C; 143 G; 237 T; 0 other;

Query Match 7.88; Score 57; DB 21; Length 834;
Best Local Similarity 100.0%; Pred. No. 1,66-14;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 519 agataaccacttaagcagcagcctctgagacatcatatcataatcaca 575
|||||
Db 618 agataaccacttaagcagcagcctctgagacatcatatcataatcaca 674

RESULT 7

AA96468
ID AAA96468 standard; DNA: 68 BP.

XX
AC AAA96468;

XX 08-FEB-2001 (first entry)

DE Nucleotide sequence of the directional building block S3.

XX petE promoter; chimeric promoter; transgenic plant; MPr1109;

KW plastocyanin gene promoter; PCR primer; ss.

XX Synthetic.

XX WO200056906-A1.

XX 28-SEP-2000.

XX 20-MAR-2000; 2000WO-1B00317

XX 22-MAR-1999; 99FR-000635.

XX (MER1-) MERISTEM THERAPEUTICS.

XX Rance I, Gruber V, Theisen M;

XX WPI; 2000-587667/55.

DR Chimeric expression promoter for producing dicotyledonous and

PT monocotyledonous transgenic plants comprises a nucleic acid sequence

PT derived from a promoter of the pea plastocyanin gene -

XX Claim 24; Page 73; 83pp; English.

XX The present sequence represents the directional building block S3,
CC which is used to construct chimeric promoters of the invention in
CC PCR reactions. The specification describes a chimeric expression
CC promoter comprising a petE promoter of the pea plastocyanin gene, or
CC comprising a G box operably or functionally linked upstream of a
CC CAAT box, TATA box and transcription initiation site. The chimeric
CC promoters are used in expression vectors for producing transgenic
CC plants, such as dicotyledonous species, e.g. potato, tobacco, cotton,
CC lettuce, tomato, melon, cucumber, pea, rape, beetroot, or sunflower,
CC and monocotyledonous species, e.g. wheat, barley, oat, rice, or corn.

XX Sequence 68 BP: 22 A; 19 C; 5 G; 22 T; 0 other;

Query Match 4.78; Score 34; DB 21; Length 68;

Best Local Similarity 100.0%; Pred. No. 8,46-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 542 cactctgtgacatcatatcataatcaca 575
|||||
Db 12 cactctgtgacatcatatcataatcaca 45

RESULT 8

AA96462
ID AAA96462 standard; DNA: 250 BP.

XX
AC AAA96462;

XX 08-FEB-2001 (first entry)

DE Nucleotide sequence of the promoter MPr1109

XX petE promoter; chimeric promoter; transgenic plant; MPr1109;

KW plastocyanin gene promoter; ss.

XX Synthetic.

XX Pisum sativum.

XX WO200056906-A1.

XX 28-SEP-2000.

XX 20-MAR-2000; 2000WO-1B00317.

XX 22-MAR-1999; 99FR-000635.

XX (MER1-) MERISTEM THERAPEUTICS.

XX Rance I, Gruber V, Theisen M;

XX WPI; 2000-587667/55.

DR Chimeric expression promoter for producing dicotyledonous and

PT monocotyledonous transgenic plants comprises a nucleic acid sequence

PT derived from a promoter of the pea plastocyanin gene -

XX Claim 2, Page 63; 83pp; English.

XX The present sequence represents the chimeric promoter MPr1109. The
CC promoter is derived from the petE promoter from pea plastocyanin gene,
CC by fusing the petE as-1 like and nos enhancer like elements to the
CC promoter MPr1098 (comprising TATA and CAAT boxes of petE), and then
CC deleting 33 bp from the 5'UTP. The petE promoter directs cell specific
CC but not full light-regulated expression in transgenic tobacco plants.
CC The promoter is used to construct chimeric promoters of the invention.
CC The specification describes a chimeric expression promoter comprising
CC a promoter of the pea plastocyanin gene, or comprising a G box operably
CC or functionally linked upstream of a CAAT box, TATA box and
CC transcription initiation site. The chimeric promoters are used in
CC expression vectors for producing transgenic plants, such as
CC dicotyledonous species, e.g. potato, tobacco, cotton, lettuce, tomato,
CC melon, cucumber, pea, rape, beetroot, or sunflower, and monocotyledonous
CC species, e.g. wheat, barley, oat, rice, or corn.

XX Sequence 250 BP: 81 A; 67 C; 31 G; 71 T; 0 other;

Query Match 4.78; Score 34; DB 21; Length 250;
Best Local Similarity 100.0%; Pred. No. 7,66-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 542 cactctgtgacatcatatcataatcaca 575
|||||
Db 91 cactctgtgacatcatatcataatcaca 124

RESULT 9

AA096460
ID AA096460 standard; UNK; 207 bp;
XX
XX
AA096460;
XX
XX 08 FEB 2001 (first entry)
XX
XX
XX Nucleotide sequence of the promoter MPT098.
XX
XX petE promoter; chinmE promoter; transgenic plant; MPT097;
XX
XX plastocyanin gene promoter; 58;
XX
XX Synthesis;
XX
XX plant sativum;
XX
XX W020056906 AL;
XX
XX 28 SEP 2000;
XX
XX 20 MAR 2000; 2000W0100047
XX
XX 22 MAR 1999; 99FR 0006635
XX
XX (MER) MERISTEM THERAPEUTICS;
XX
XX Kance I, Gribbet V, Therrien M;
XX
XX W01 2000 587667255;
XX
XX chinmE expression promoter for producing a polyphenolic and
XX
XX monochlorophenous transgenic plants comprises a nucleic acid sequence
XX
XX derived from a promoter of the pea plastocyanin gene
XX
XX (claim 2); Page 6/7; Bippy English
XX
XX
XX The present sequence represents the chinmE promoter MPT098. The
XX
XX promoter is derived from the petE promoter from pea plastocyanin gene,
XX
XX and contains only the TATA and CAT boxes, and corresponds to a
XX
XX minimal reference promoter on the petE promoter. The petE promoter
XX
XX directs cell specific but not full light-regulated expression in
XX
XX transgenic tobacco plants. The promoter is used to construct chinmE
XX
XX promoters of the invention. The specification describes a chinmE
XX
XX expression promoter consisting a promoter of the pea plastocyanin gene
XX
XX of comprising a 6 box operability or functionality linked upstream of a CAT
XX
XX box, TATA box and transcription initiation site. The chinmE promoters
XX
XX are used in expression vectors for producing transgenic plants, such as
XX
XX dicotyledonous species, e.g. potato, tobacco, cotton, lettuce, tomato,
XX
XX mungbean, pea, lupin, beet root, or sunflower, and monocotyledonous
XX
XX species, e.g. wheat, barley, oat, rice, corn, or sorghum.
XX
XX
XX Sequence 207 bp; 6/7; A: 138 C: 21 G: 61 T: 0 other:
XX

	Query Match	4.48%	Score 42	JB 21	Length 207
	Host Local Similarity	100.00%	Freq. No. 0.00054		
	Motifpos	42	Conservation	-	Mismatches 0; Indels 0; Gaps 0
QY	544 ctctgtgagacatcctcatctatccaaaccca	5/5			
	[] [] [] [] []				
Ibb	16 ctctgtgagacatcctcatctatccaaaccca	4/7			
RE:SMT.F	10				
	AAA9646.3				
(1)	AAA9646.3 standard; DNA; 280 bp.				
XX					
A'	AAA9646.3;				
XX					
D1	08 FEM 2001 (first entry)				
XX					
note	Nucleotide sequences of the promoter Mpr1110.				
XX					
W	pMPrE promoter; ethylene promoter; transactivator plant; Mpr1110?				

KM	plastocyanin gene promoter, ss
XX	
06	Synthetic,
08	pisum sativum,
XX	
FN	W0200056906 A1.
XX	
FD	28 SEP-2000.
XX	
PF	29 MAR-2000; 2000WO/1H03-17.
XX	
PR	22 MAR-1999; 99FE-0004635.
XX	
PA	(MERI) MERISTEM THERAPEUTICS.
XX	
P1	Rance I, Gruber V, Theissen M;
XX	WE1; 2000 587667/55.
DR	
PT	Chimeric expression promoter for producing dicotyledonous and
PP	monocotyledonous Transgenic plants comprises a nucleic acid sequence
XX	derived from a promoter of the pea plastocyanin gene
XX	
PS	claim 2; page 70; 8pp; English.
XX	
CC	The present sequence represents the chimeric promoter Mp1110. The
CC	promoter is derived from the pea promoter from pea Plastocyanin gene,
CC	by fusing the peptide as 1 like and non-exchangeable like elements to the
CC	promoter Mp1098 (comprising TATA and CAAT boxes of pea), and then
CC	inserting a G box and joining a truncated 35S RNA of CMV. The pea
CC	promoter directs cell-specific but not full light regulated expression in
CC	transgenic tobacco plants. The promoter is used to construct chimeric
CC	promoters of the invention. The specification describes a chimeric
CC	expression promoter comprising a promoter of the pea plastocyanin gene,
CC	or comprising a G box operably or functionally linked upstream of a CAAT
CC	box, TATA box and transcription initiation site. The chimeric promoters
CC	are used in expression vectors for producing transgenic plants, such as
CC	dicotyledonous species, e.g. potato, tobacco, cotton, lettuce, tomato,
CC	melon, cucumber, pea, rape, beetroot, or sunflower, and monocotyledonous
CC	species, e.g. wheat, barley, oat, rice, or corn
XX	
SD	Sequence 283 BF; 88 A; 74 C; 42 G; 77 T; 0 other
Query Match	4.2%
Best Local Similarity	100.0%; Prod. No. 0.0014.
Matches	41; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
54.	GACTGTGTCACATCATTTATCATTATCAGT 5/12
68	CACCTTGTCACATCATTTATCAGT 98
30	

RESULT 11	
AAA96465	
ID	AAA96465 standard; tRNA; 296 bp
XX	
AC	AAA96465;
XX	
D7	08-FEB-2001 (first entry)
XX	
DE	Nucleotide sequence of the promoter M71111.
XX	
KW	Putative promoter; chemoic promoter; transactivator; M71111;
KW	placoyanin gene promoter; ss.
XX	
OS	Synthetic
OS	plasmid salivum.
XX	
IN	W02C0056306-A1.
XX	
PD	28-SEP-2000.
XX	

PF 20-MAR-2000: 2000WO-1B00317.
 XX
 PR 22-MAR-1999: 99PR-0003635.
 XX
 PA (MERI-) MERISTEM THERAPEUTICS
 XX
 PI Rance I, Gruber V, Theisen M;
 XX
 DR WPI: 2000-587667/55.
 XX
 PT Chimeric expression promoter for producing dicotyledonous and
 PT monocotyledonous transgenic plants comprises a nucleic acid sequence
 PT derived from a promoter of the pea plastocyanin gene
 PS Claim 2; Page 71; 83pp, English.
 XX
 CC The present sequence represents the chimeric promoter Mpr111. The
 CC promoter is derived from the pete promoter from pea plastocyanin gene,
 CC by fusing the pete as-1 like and nos enhancer like elements to the
 CC promoter Mpr1098 (comprising TATA and CAAT boxes of pete), and then
 CC inserting a G box and fusing a fragment comprising a duplication of the
 CC element as2 and as1. The pete promoter directs cell-specific but not
 CC full light-regulated expression in transgenic tobacco plants. The
 CC promoter is used to construct chimeric promoters of the invention. The
 CC specification describes a chimeric expression promoter comprising a
 CC promoter of the pea plastocyanin gene, or comprising a G box operably
 CC or functionally linked upstream of a CAAT box, TATA box and transcription
 CC initiation site. The chimeric promoters are used in expression vectors
 CC for producing transgenic plants, such as dicotyledonous species,
 CC e.g. potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea,
 CC rape, beetroot, or sunflower, and monocotyledonous species, e.g. wheat,
 CC barley, oat, rice, or corn.
 XX
 SQ Sequence 296 BP; 94 A; 74 C; 45 G; 83 T; 0 other;

Query Match 4.2%; Score 31; DB 21; Length 296;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 542 cactctgtgacacatcatatctaatac 572
 ||||||||||||||||||||||||||||
 DB 84 cactctgtgacacatcatatctaatac 114

RESULT 12
 AAA96464
 ID AAA96464 standard; DNA; 303 BP.
 XX
 AC AAA96464;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Nucleotide sequence of the promoter Mpr1153.
 XX
 KW pete promoter; chimeric promoter; transgenic plant; Mpr1153;
 KM plastocyanin gene promoter; ss.
 XX
 OS Synthetic.
 OS Pisum sativum.
 XX
 PN WO200056906-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 20-MAR-2000: 2000WO-1B00317.
 XX
 PR 22-MAR-1999: 99PR-0003635.
 XX
 PA (MERI-) MERISTEM THERAPEUTICS.
 XX
 PI Rance I, Gruber V, Theisen M;
 XX

DR WPI: 2000 587667/55.
 XX
 PT Chimeric expression promoter for producing dicotyledonous and
 PT monocotyledonous transgenic plants comprises a nucleic acid sequence
 PT derived from a promoter of the pea plastocyanin gene
 PS Claim 2; Page 70; 83pp; English.
 XX
 CC The present sequence represents the chimeric promoter Mpr1153. The
 CC promoter is derived from the pete promoter from pea plastocyanin gene.
 CC The pete promoter directs cell-specific but not full light-regulated
 CC expression in transgenic tobacco plants. The promoter is used to
 CC construct chimeric promoters of the invention. The specification
 CC describes a chimeric expression promoter comprising a promoter of the
 CC pea plastocyanin gene, or comprising a G box operably or functionally
 CC linked upstream of a CAAT box, TATA box and transcription initiation
 CC site. The chimeric promoters are used in expression vectors for producing
 CC transgenic plants, such as dicotyledonous species, e.g. potato, tobacco,
 CC cotton, lettuce, tomato, melon, cucumber, pea, rape, beetroot, or
 CC sunflower, and monocotyledonous species, e.g. wheat, barley, oat, rice,
 CC or corn.
 XX
 SQ Sequence 303 BP; 101 A; 78 C; 41 G; 84 T; 0 other;

Query Match 4.2%; Score 31; DB 21; Length 303;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 542 cactctgtgacacatcatatctaatac 572
 ||||||||||||||||||||||||||||
 DB 91 cactctgtgacacatcatatctaatac 121

RESULT 13
 AAA96470
 ID AAA96470 standard; DNA; 72 BP.
 XX
 AC AAA96470;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Nucleotide sequence of the directional building block S5.
 XX
 KW pete promoter; chimeric promoter; transgenic plant; Mpr1108;
 KM plastocyanin gene promoter; PCR primer; ss.
 XX
 OS Synthetic.
 OS
 PN WO200056906-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 20-MAR-2000: 2000WO-1B00317.
 XX
 PR 22-MAR-1999: 99PR-0003635.
 XX
 PA (MERI-) MERISTEM THERAPEUTICS.
 XX
 PI Rance I, Gruber V, Theisen M;
 XX
 DR WPI: 2000-587667/55.
 XX
 PT Chimeric expression promoter for producing dicotyledonous and
 PT monocotyledonous transgenic plants comprises a nucleic acid sequence
 PT derived from a promoter of the pea plastocyanin gene
 PS Claim 24, Page 75; 83pp, English.
 XX
 CC The present sequence represents the directional building block S5,
 CC which is used to construct chimeric promoters of the invention in
 CC PCR reactions. The specification describes a chimeric expression
 CC promoter comprising a pete promoter of the pea plastocyanin gene, or

Search completed: September 1, 2002, 03:16:38
Job time: 8287 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd

OM nucleic - nucleic search, using sw model

Run on: September 1, 2002, 01:57:53 : Search time 1226.08 seconds
(without alignments)
3058.286 Million cell updates/sec

Title: US-09-678-303-3
Perfect score: 731
Sequence: 1 agagagagagagagagagagag 3' aatcatttggagagagag 731

Scoring table:
OLIGO_MUC
Gapop 60 0 0 Gapext 60 0

Searched: 13736207 seqs, 674847542 residues

Word size: 0

Total number of hits satisfying chosen parameters: 2742414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

EST:
1: em_estha:
2: em_estlum:
3: em_estnu:
4: em_estnu:
5: em_estnu:
6: em_estnu:
7: em_estnu:
8: em_estnu:
9: gb_estl:
10: gb_estl:
11: gb_estl:
12: gb_estl:
13: em_gss_hum:
14: em_gss_hum:
15: em_gss_hum:
16: em_gss_vrt:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	39	5.3	376	10	HE45678 NP04909
2	39	4.8	611	10	HE45678 NP04909
3	29	4.0	263	9	AM692408 NP050108
4	29	4.0	341	10	BE316266 NP034931
5	29	4.0	369	10	BE316266 NP034931
6	29	4.0	376	10	HE45678 NP04909
7	29	4.0	483	10	HE45678 NP04909
8	29	4.0	603	9	AM692408 NP050108
9	29	4.0	611	10	HE45678 NP04909
10	29	4.0	637	10	HE45678 NP04909
11	29	4.0	645	10	BE316266 NP034931
12	29	4.0	683	10	BE316266 NP034931
13	29	3.8	223	10	BE316266 NP034931
14	28	3.8	354	9	AM692408 NP050108
15	28	3.8	468	12	AO841643 NP031613
16	27	3.7	340	10	BE316266 NP034931
17	27	3.7	514	10	BE316266 NP034931

18	27	3.7	737	10	BE094026
19	27	3.7	774	10	BE398417
20	26	4.4	518	10	HE317607
21	25	3.4	159	10	HE317607
22	25	3.4	174	10	HE317607
23	25	3.4	334	9	AM777001
24	25	3.4	337	9	AM777001
25	25	3.4	446	9	AM777001
26	25	3.4	351	10	HE317607
27	25	3.4	351	10	HE317607
28	25	3.4	351	10	HE317607
29	25	3.4	351	10	HE317607
30	25	3.4	351	10	HE317607
31	25	3.4	351	10	HE317607
32	25	3.4	351	10	HE317607
33	25	3.4	351	10	HE317607
34	25	3.4	351	10	HE317607
35	25	3.4	351	10	HE317607
36	25	3.4	351	10	HE317607
37	25	3.4	351	10	HE317607
38	25	3.4	351	10	HE317607
39	25	3.4	351	10	HE317607
40	25	3.4	351	10	HE317607
41	25	3.4	351	10	HE317607
42	25	3.4	351	10	HE317607
43	25	3.4	351	10	HE317607
44	25	3.4	351	10	HE317607
45	25	3.4	351	10	HE317607

ALIGNMENTS

RESULT 1	BE635678	376 bp	mRNA	linear	EST 19-DEC-2000
LOCUS	BE635678				
DEFINITION	BE635678				
ACCESSION	BE635678				
VERSION	BE635678				
KEYWORDS	EST				
SOURCE	barrel medic.				
ORGANISM	Medicago truncatula				
REFERENCE	1 (bases 1 to 376)				
AUTHORS	Torres, Jerez, L., Scott, A. B., Harris, A. B., Gonzalez, K. A., Bell, C. J., Flores, H. P., Imman, J. T., Welton, J. W., and May, G. D.				
TITLE	Expressed Sequence Tags from the Samuel Roberts Noble Foundation				
JOURNAL	Medicago truncatula drought library				
COMMENT	Unpublished (2000)				
	Contact: May GD				
	Plant Biology Division				
	The Samuel Roberts Noble Foundation				
	2510 East Noble Parkway, Ardmore, OK 73402, USA				
	Tel.: 580 221 7391				
	Fax: 580 221 7380				
	Email: jmay@noble.org				
	Insert Length: 376				
	Insert Size: 0.00				
	Plate: 100				
	Seq primer: 10CACACACACACACACACACAC				
	Location: 100				
	1, 376				
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source					
	/organism="Medicago truncatula"				
	/db="EST"				
	/accession="BE635678"				
	/version="NP04909"				
	/key="EST"				
	/note="Vector: Lambda Zap; contains a mixture of end-labeled plasmids harvested in a series of days-post-infection"				

REFERENCE 1 (bases 1 to 341)
 AUTHORS Torres-Jerez, I., Scott, A. B., Harris, A. R., Gonzales, R. A., Bell, C. J., Flores, H. P., Imman, J. T., Weller, J. W. and May, G. D.
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 JOURNAL Medicago truncatula leaf library
 COMMENT Unpublished (2000)
 On Jul 14, 2000 this sequence was refiled as refseq-191-056043.
 CONTACT: May GD
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7391
 Fax: 580 221 7380
 Email: gdmay@noble.org
 Medicago Genome Initiative accession: MGI:S18233
 Insert Length: 876, Std Error: 0.00
 Plate: 035, row: F, column: 01
 Seq primer: TCACGACCAAGACGACTAATGAC
 Location/Qualifiers
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 /db_xref="taxon:3880"
 /clone_lib="Developing leaf"
 /issue_type="leaf"
 /dev_stage="Pooled developmental"
 /note="Vector: lambda Zap; Contains a mixture of very young, developing, mature and senescing leaves."

BASE COUNT 90 a 81 c 73 g 97 t

ORIGIN

Query Match 4.0%; Score 29; DB 10; Length 341;
 Best Local Similarity 100.0%; Pred. No. 5;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 678 acacatacaaaagaaagaaactaat 706
 |||||||
 Db 16 ACACATACAAAGACGACGACTAAT 44

RESULT 5
 BI272586 369 bp mRNA linear EST 18 JUL 2001
 LOCUS NF00236211F1047 Developing flower Medicago truncatula cDNA clone
 DEFINITION NF00236211F1047, mRNA sequence.
 ACCESSION BI272586
 VERSION BI272586.1 GI:1487866
 KEYWORDS barrel medic.
 SOURCE Medicago truncatula
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicotyledons; Rosidae; eucosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.
 1 (bases 1 to 359)
 Torres-Jerez, I., Scott, A. B., Harris, A. R., Gonzales, R. A., Bell, C. J., Flores, H. P., Imman, J. T., Weller, J. W. and May, G. D.
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 JOURNAL Medicago truncatula flower library
 COMMENT Unpublished (2001)
 CONTACT: May GD
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7391
 Fax: 580 221 7380
 Email: gdmay@noble.org
 Insert Length: 369, Std Error: 0.00
 Plate: 022, row: H, column: 05
 Seq primer: TCACGACCAAGACGACTAATGAC
 Location/Qualifiers

FEATURES

source 1..369
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone_lib="Developing flower"
 /issue_type="Developing flowers"
 /dev_stage="Developmentally pooled; Contains a mixture of very young, developing, fully opened flowers and flowers in early transition into pods."
 /note="Vector: lambda zap; cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from very young, developing, fully opened flowers and flowers transitioning into pods. The cDNA was directionally ligated into the Zap XR vector (Stratagene) and packaged using the GigaPack III Gold packaging extracts. Phagocids containing cDNA inserts were in vivo excised from the phagecoat DNA. The phage coat was using EXASist helper phage and the E. coli strain XL1-blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."

BASE COUNT 100 a 87 c 78 g 102 t 2 others

ORIGIN

Query Match 4.0%; Score 29; DB 10; Length 369;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 678 acacatacaaaagaaagaaactaat 706
 |||||||
 Db 25 ACACATACAAAGACGACGACTAAT 53

RESULT 6
 BI270865 378 bp mRNA linear EST 18 JUL 2001
 LOCUS NF00236211F1020 Developing flower Medicago truncatula cDNA clone
 DEFINITION NF00236211F1020, mRNA sequence.
 ACCESSION BI270865
 VERSION BI270865.1 GI:1487866
 KEYWORDS barrel medic.
 SOURCE Medicago truncatula
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicotyledons; Rosidae; eucosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.
 1 (bases 1 to 378)
 Torres-Jerez, I., Scott, A. B., Harris, A. R., Gonzales, R. A., Bell, C. J., Flores, H. P., Imman, J. T., Weller, J. W. and May, G. D.
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 JOURNAL Medicago truncatula flower library
 COMMENT Unpublished (2001)
 CONTACT: May GD
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7391
 Fax: 580 221 7380
 Email: gdmay@noble.org
 Insert Length: 378, Std Error: 0.00
 Plate: 002, row: G, column: 02
 Seq primer: TCACGACCAAGACGACTAATGAC
 Location/Qualifiers
 1..378
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone_lib="Developing flower"
 /issue_type="Developing flowers"
 /dev_stage="Developmentally pooled; Contains a mixture of very young, developing, fully opened flowers and flowers in early transition into pods."

FEATURES

BASE CATALYST	101 a	101 b	102 a
TRIGLYCIN	101 c	101 d	102 b

Cy	b78	a c a c a t a c c a a g a q a a q a q o c i a n f e b d l
Ile	44	A A C A A I A F A A A C G A N A u G A A v T S A L P A A V

CRITICISM

CONFIDENTIAL: MAY 17
PLANT BIOLOGY DIVISION

PLAINTS

Section

1000100/0000 110000

4000

WASTE, OTHER	1.12	95	144
COLLECTIN	143	4	4

Query Match	4	8	Score 29	100	100	100	48
Post Local Similarity	100	100	Prod. No. 4				
Matches 29	Corrective		Matches	0	Index	0	Output

678 AGGATACGAGGCTGGAGAGGAGTAAATGTTT
 679 | | | | | | | | | | | | | | | | | |
 680 AAAATATACAAATACCAACAGCAATAAATTAATTAAT

Accession	Size (bp)	mRNA	Insertion	Position
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U06301	201	100%	100%	100%
U06302	201	100%	100%	100%
U06303	201	100%	100%	100%
U06304	201	100%	100%	100%
U06305	201	100%	100%	100%
U06306	201	100%	100%	100%
U06307	201	100%	100%	100%
U06308	201	100%	100%	100%
U06309	201	100%	100%	100%
U06310	201	100%	100%	100%
U06311	201	100%	100%	100%
U06312	201	100%	100%	100%
U06313	201	100%	100%	100%
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U06322	201	100%	100%	100%
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U06326	201	100%	100%	100%
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U06371	201	100%	100%	100%
U06372	201	100%	100%	100%
U06373	2			

ACCESSION	AW692904
VERSION	AW692904.2 (1:1) 113654
REPEATING UNIT	

KEYWORDS	PSI.
SOLUBLE	patrol medic.
ORGANISM	Modicare + modatol

REFERENCE
1 (basos 1 to 604)
Ho, X.-Z., Shadiev, G., Scott, A. D., Harris, A. R., Muzalovs, R. A., [et al.]

TITLE	Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicinal Plant Data Library
JOURNAL	NCBI (2000)
COMMENT	on Apr 14, 2000 this sequence version replaced at 156,744.

Dr. Samuel Roberts Noble Foundation
2110 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel.: 580 221 7402
Fax: 580 221 7480
Email: info@noble.org
Internet: www.noble.org
Established: 6/76 Seed Pot: 0.00
Fido: 060 FOW: 5 Column: 12
Seq primer: TCNANATGAAATGATGATG

FEATURES	SOURCE	Location/Qualifiers
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		/ab_x: "taxon: 4880"
		/ab_x: "N060612ST"
		/ab_x: "Theve" "Popul stem"
		/ab_x: "Type" "stem"
		/ab_x: "Stem" "Popul decol" "mentat"
		/ab_x: "Stem" "Lambada" "Zap" "Cortinas" "a mixture of"
		intermodal stem "stem" "S"
BASE COUNT		164
ORIGIN		141 a 128 a 180 t

[illegible][illegible]

MODICUM Modicidae, Trichostoma
Eukaryota: Viridiplantae, Streptophyta, Embryophyta: Tracheophyta
Spermatophyta: Magnoliophyta, eudicotyledons, core eudicotS?

Rosidae: eucosids I: Fabales, Fabaceae, Papilionoideae: Trifoliaceae: Medicago.

1 (bases 1 to 611)

Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Holl, C.J., Flores, H.R., Imman, J.T., Weller, J.W., and May, G.D.,
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula leaf library
Unpublished (2000)

JOURNAL
COMMENT On Jul 13, 2000 this sequence version replaced g1:9119403.

CONTACT: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org

Medicago Genome Initiative accession: MG1:S:15181
Insert Length: 657 Std Error: 0.00
Plate: 020 Row: B Column: 11
Seq primer: TCACACACGAAACACCTATATAC

FEATURES
Source
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/db_xref="taxon:3880"
/clone="NF020B11LP"
/clone_lib="Developing leaf"
/tissue_type="leaf"
/dev_stage="Pooled developmental"
/note="Vector, lambda Zap, contains a mixture of very young, developing, mature and senescing leaves"

BASE COUNT
ORIGIN
164 a 138 c 132 g 177 t

Query Match 4.0% Score 29; DB 10; Length 611;
Best Local Similarity 100.0%; Pred No. 3.5; Mismatches 0; Indels 0; Gaps 0;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 678 acacatacaagaagaagactaatat 706
|||||
DB 34 ACACATACAAAGACAGACTATATAT 62

RESULT 10
BG4:7563 637 bp mRNA linear EST 19-MAR-2001
LOCUS NF105G07P1P1054 Phosphate starved leaf Medicago truncatula cDNA
DEFINITION
ACCESSION BG457563
VERSION BG457563.1 GI:13480804
KEYWORDS EST
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eucosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
1 (bases 1 to 637)
Liu, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W., May, G.D., and Harrison, M.T.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula phosphate-starved leaf library
Unpublished (2000)

JOURNAL
COMMENT Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
Email: mtharrison@noble.org
Insert Length: 637 Std Error: 0.00
Plate: 105 Row: G Column: 07
Seq primer: TCACACGAAACACCTATATAC

FEATURES
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1..637
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF014C09LP"
/clone_lib="Phosphate starved leaf"
/tissue_type="leaf"
/dev_stage="Trifoliolate"
/note="Vector, lambda Zap; At the trifoliolate stage, M truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days, during this 30 day period the plants were fertilized with 0.1% 100 mg/L potassium phosphate. RNA was prepared from above ground tissues."

BASE COUNT
ORIGIN
178 a 148 c 128 g 182 t

Query Match 4.0% Score 29; DB 10; Length 645;
Best Local Similarity 100.0%; Pred No. 3.4; Mismatches 0; Indels 0; Gaps 0;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 678 acacatacaagaagaagactaatat 706
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DB 88 ACACATACAAAGACAGACTATATAT 116

RESULT 11
BE249343 645 bp mRNA linear EST 13-JUN-2000
LOCUS NF014C09LP1069 Developing leaf Medicago truncatula cDNA clone
DEFINITION
ACCESSION BE249343
VERSION BE249343.1 GI:9119403
KEYWORDS EST
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eucosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
1 (bases 1 to 645)
Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W., and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula leaf library
Unpublished (2000)

JOURNAL
COMMENT Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Medicago genome initiative accession: MG1:S:14891
Insert Length: 645 Std Error: 0.00
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Seq primer: TCACACGAAACACCTATATAC

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/clone_lib="Developing leaf"
/tissue_type="leaf"
/dev_stage="Pooled developmental"
/note="Vector, lambda Zap, contains a mixture of very young, developing, mature and senescing leaves."

BASE COUNT
ORIGIN
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Query Match 4.0% Score 29; DB 10; Length 645;


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/organism="Medicago truncatula"
/cultivar="genotype A17"
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/clone="72-F-02-084"
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Job time: 10703 sec

OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/826,439
FILING DATE:
CLASSIFICATION: 510
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 03/424,641
FILING DATE: April 19, 1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ian G. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: Quest 4 1-155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
TELEX: No. 5972674e
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2987 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE:
US-08-826-439-1

Query Match 2.58; Score 19; DH 2; Length 2987;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 267 atgaattgataaagaatt 285
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Db 1446 ATCAATTGATCAAGACTT 1464

RESULT 5
US-08-913-159-1
Sequence 1, Application US/08913159
Patent No. 6300109
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Plasmid-derived type II
TITLE OF INVENTION: restriction-modification systems from *Lactococcus lactis*
NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EP)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,159
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0179/95
FILING DATE: 17-FEB-1995
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3695 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: *Lactococcus lactis* subsp. *cremoris*
STRAIN: W9
FEATURE:
NAME/KEY: CDS
LOCATION: 769..1620
IDENTIFICATION METHOD: experimental

OTHER INFORMATION: /codon_start- 769
OTHER INFORMATION: /product- "L1A1-GATC- N-6-adenine methylase A"
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FEATURE:
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FEATURE:
NAME/KEY: CDS
LOCATION: 2412..3323
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /codon_start- 2412
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US-08-913-159-1

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 267 atgaattgataaagaatt 285
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Db 2118 ATCAATTGATCAAGACTT 2136

RESULT 6
US-08-913-159-3
Sequence 3, Application US/08913159
Patent No. 6300109
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Plasmid-derived type II
TITLE OF INVENTION: restriction modification systems from *Lactococcus lactis*
NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EP)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,159
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0179/95
FILING DATE: 17-FEB-1995
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3695 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: *Lactococcus lactis* subsp. *cremoris*

every Match	2.08	Score 19:	138.4	Length	46.9%
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Matched	19;	Connective	04;	Tuple	0;
		Mismatch	04;	Map	0;

DES011 9
 PAT 0801 0080 156
 Sequence 156, Application 147148910600
 GENERAL INFORMATION:
 APPLICANT: MATTOCK, Mark D
 APPLICANT: Mattock, Steven
 TITLE OF INVENTION: STUDENT'S STRIKE NONHOMOGENEOUS
 TITLE OF INVENTION: STUDENT'S STRIKE NONHOMOGENEOUS
 TITLE OF INVENTION: STUDENT'S STRIKE NONHOMOGENEOUS
 NUMBER OF SEQUENCE: 198
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/03680
FILING DATE: 19910524
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4610-0011.40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ. ID NO: 156:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
PCT-JS91-03680-156

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Best Local Similarity 100.0%; Pred. No. 66;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 AGAGAGAAAAGAGAGAG 22

RESULT 10
US-08-378-588-15
Sequence 15, Application US/08378588
Patent No. 5608148
GENERAL INFORMATION:
APPLICANT: John, Maliyakal E.
TITLE OF INVENTION: TRANSGENIC COTTON PLANTS
TITLE OF INVENTION: PRODUCING HETEROLOGOUS PEROXIDASE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nicholas J. Seay, Quarles & Brady
STREET: First Wisconsin Plaza, One South
STREET: Pinckney St.,
STREET: P.O. Box 2113
CITY: Madison
STATE: WI
COUNTRY: USA
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,588
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 11-229-9101 2
TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 251-2484
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ. ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1064 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-378-588-15

Query Match 2.5%; Score 18; DB 1; Length 1064;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 699 taattaattaataatca 716
|||||

Db 785 TAATTAATTAATTAATCA 802

RESULT 11
US-08-811-094-15
Sequence 15, Application US/08811094
Patent No. 5869720
GENERAL INFORMATION:
APPLICANT: John, Maliyakal E.
TITLE OF INVENTION: TRANSGENIC COTTON PLANTS
TITLE OF INVENTION: PRODUCING HETEROLOGOUS PEROXIDASE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nicholas J. Seay, Quarles & Brady
STREET: First Wisconsin Plaza, One South
STREET: Pinckney St.,
STREET: P.O. Box 2113
CITY: Madison
STATE: WI
COUNTRY: USA
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,094
FILING DATE: 03-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/378,588
FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 11-229-9101-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-2484
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ. ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1064 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-811-094-15

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Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 699 taattaattaataatca 716

10b 785 TAAATAAATAAATAAATA 802

RESULT 12
1 US-08-11121-15

2 Sequence 15, Application US/08-11121

3 GENERAL INFORMATION:

4 APPLICANT: John, Mallyakal E.

5 TITLE OF INVENTION: TRANSGENIC COTTON PLANTS

6 TITLE OF INVENTION: PRODUCING HETEROLOGOUS PROXIMASE

7 NUMBER OF SEQUENCES: 24

8 CORRESPONDENCE ADDRESS:

9 ADDRESS: Nicholas J. Seay, Quatles & Brady

10 STREET: First Wisconsin Plaza, One South

11 STREET: Pinckney St.

12 STREET: P.O. Box 2113

13 CITY: Madison

14 STATE: WI

15 COUNTRY: USA

16 ZIP: 53701 2113

17 COMPUTER READABLE FORM:

18 MEDIUM TYPE: Floppy disk

19 COMPUTER: IBM PC compatible

20 OPERATING SYSTEM: PC DOS/MS DOS

21 SOFTWARE: Patent In Release #1.0, Version #1.25

22 CURRENT APPLICATION DATA:

23 APPLICATION NUMBER: P01/28394/21121

24 FILING DATE:

28 CLASSIFICATION:

29 ATTORNEY/AGENT INFORMATION:

30 NAME: Seay, Nicholas J.

31 REGISTRATION NUMBER: 27,486

32 REFERENCE/BOOK NUMBER: 11 229 9101-2

33 TELECOMMUNICATION INFORMATION:

34 TELEPHONE: (608) 251-2484

35 TELEFAX: (608) 251-9166

36 INFORMATION FOR SEQ ID NO: 15

37 SEQUENCE CHARACTERISTICS:

38 LENGTH: 1064 base pairs

39 TYPE: nucleic acid

40 STRANDEDNESS: double

41 TOPOLOGY: linear

42 MOLECULE TYPE: cDNA

43 PRT US04 11121 15

Query Match 2.5% Score 18; LB 5; Length 1064;
Post Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 699 TAAATAAATAAATAAATA 716

10b 785 TAAATAAATAAATAAATA 802

RESULT 13
1 US-08-378-588-23

2 Sequence 23, Application US/08-378588

3 Patent No. 5608148

4 GENERAL INFORMATION:

5 APPLICANT: John, Mallyakal E.

6 TITLE OF INVENTION: TRANSGENIC COTTON PLANTS

7 NUMBER OF SEQUENCES: 29

8 CORRESPONDENCE ADDRESS:

9 ADDRESS: Nicholas J. Seay, Quatles & Brady

10 STREET: First Wisconsin Plaza, One South

11 STREET: Pinckney St.

12 STREET: P.O. Box 2113

13 CITY: Madison

14 STATE: WI

15 COUNTRY: USA

ZIP: 53701 2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08-378,588
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,486
REFERENCE/BOOK NUMBER: 11 229 9101-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-2484
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1270 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-378-588-23

Query Match 2.5% Score 18; LB 1; Length 1270;
Post Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 699 TAAATAAATAAATAAATA 716

10b 991 TAAATAAATAAATAAATA 1008

RESULT 14
1 US-08-811-094-23

2 Sequence 23, Application US/08811094

3 Patent No. 5869720

4 GENERAL INFORMATION:

5 APPLICANT: John, Mallyakal E.

6 TITLE OF INVENTION: TRANSGENIC COTTON PLANTS

7 NUMBER OF SEQUENCES: 29

8 CORRESPONDENCE ADDRESS:

9 ADDRESS: Nicholas J. Seay, Quatles & Brady

10 STREET: First Wisconsin Plaza, One South

11 STREET: Pinckney St.

12 STREET: P.O. Box 2113

13 CITY: Madison

14 STATE: WI

15 COUNTRY: USA

16 ZIP: 53701 2113

17 COMPUTER READABLE FORM:

18 MEDIUM TYPE: Floppy disk

19 COMPUTER: IBM PC compatible

20 OPERATING SYSTEM: PC DOS/MS DOS

21 SOFTWARE: Patent In Release #1.0, Version #1.25

22 CURRENT APPLICATION DATA:

23 APPLICATION NUMBER: US/08-811,094

24 FILING DATE: 03 MAR 1997

25 CLASSIFICATION: 800

26 PRIOR APPLICATION DATA:

27 APPLICATION NUMBER: 08/378,588

28 FILING DATE: 25 JAN 1995

29 ATTORNEY/AGENT INFORMATION:

30 NAME: Seay, Nicholas J.

31 REGISTRATION NUMBER: 27,486

32 REFERENCE/BOOK NUMBER: 11 229 9101-2

33 TELECOMMUNICATION INFORMATION:

34 TELEPHONE: (608) 251-2484

35 TELEFAX: (608) 251-9166

Job time: 8.235 sec

? INFORMATION FOR SEQ ID NO: 23:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 1270 base pairs
 ? TYPE: nucleic acid
 ? STRANDEDNESS: double
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: DNA (genomic)
 ? US-08-81-094-23

Query Match 2.5%; Score 18; DB 2; Length 1270;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Oy 699 taattaataataatca 716
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 Db 991 TAATTAATTAATTAATCA 1008

RESULT 15
 PCT-US94-11121-23
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 ? GENERAL INFORMATION:
 ? APPLICANT: John, Mallyakal E.
 ? TITLE OF INVENTION: TRANSGENIC COTTON PLANTS
 ? TITLE OF INVENTION: PRODUCING HYPEROLGOLUS PEROXIDASE
 ? NUMBER OF SEQUENCES: 23
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Nicholas J. Seay, Charles & Brady
 ? STREET: First Wisconsin Plaza, One South
 ? STREET: Pinckney St.
 ? STREET: P.O. Box 2113
 ? CITY: Madison
 ? STATE: WI
 ? COUNTRY: USA
 ? ZIP: 53701-2113
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent in Release #1.0, Version #1.25
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: PCT/US94/11121
 ? FILING DATE:
 ? CLASSIFICATION:
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Seay, Nicholas J.
 ? REGISTRATION NUMBER: 27,386
 ? REFERENCE/DOCKET NUMBER: 11-229-9076-8
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (608) 251-2484
 ? TELEFAX: (608) 251-9166
 ? INFORMATION FOR SEQ ID NO: 23:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 1270 base pairs
 ? TYPE: nucleic acid
 ? STRANDEDNESS: double
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: DNA (genomic)
 ? PCT-US94-11121-23

Query Match 2.5%; Score 18; DB 5; Length 1270;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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